

PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24-
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 28
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-2442-074-28

Query Match 84.6%; Score 899; DB 12; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.1e-12;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-2442-074-28

Qy 32 MEKIPVSAFLLVASYTLLARDTVKPGAKKDTKDSRKLPOTLSRGWDOLINTOTYEE 91
 Db 1 MBKIPVSAFLLVASYTLLARDTVKPGAKKDTKDSRKLPOTLSRGWDOLINTOTYEE 60

Qy 92 ALYKSNTSNKPLMIIHLDCEPHSQAQLKKVFAENKEIQKLAEQFVLNLVETTDKLSP 151
 Db 61 ALYKSNTSNKPLMIIHLDCEPHSQAQLKKVFAENKEIQKLAEQFVLNLVETTDKLSP 120

Qy 152 DQGYVPRIMFDPSLTVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL 206
 Db 121 DQGYVPRIMFDPSLTVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL 175

RESULT 6
 US-10-242-574-28
 Sequence 28. Application US/10242574
 Publication No. US20030138899A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watane, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630R1C20
 CURRENT APPLICATION NUMBER: US/10/242,574
 CURRENT FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/090557

RESULT 5
 US-10-242-505-28
 Sequence 28. Application US/10242505
 Publication No. US20030138899A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watane, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630R1C25
 CURRENT APPLICATION NUMBER: US/10/242,505
 CURRENT FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 PRIOR FILING DATE: 1998-06-25
 REMAINING PRIORITY Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 28
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-243-261-28

Query Match 84.6%; Score 899; DB 12; Length 175;
 Best Local Similarity 100%; Pred. No. 2.1e-92;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSAFLLLVALSNTLARDTIVKGAKKDTKDSRKLPOTLSRGNGDQLWTQTYEE 91
 Db 1 MEKIPVSAFLLLVALSNTLARDTIVKGAKKDTKDSRKLPOTLSRGNGDQLWTQTYEE 60

Qy 92 ALYKSKTNSNPKLMIHHHDECPHSQALKVFAENKEOKLAEOFVLLNVYETTDKLSP 151
 Db 61 ALYKSKTNSNPKLMIHHHDECPHSQALKVFAENKEOKLAEOFVLLNVYETTDKLSP 120

Qy 152 DGOYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
 Db 121 DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 175

RESULT 8
 US-10-243-282-28
 Sequence 28, Application US/10243282
 Publication No. US20030138901A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watanabe, Collin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630R1C50

CURRENT APPLICATION NUMBER: US/10/243-282
 CURRENT FILING DATE: 2002-09-13
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: P3630R1C50
 PRIOR FILING DATE: 1998-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 28
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-243-282-28

Remaining Priority Application data removed - See File Wrapper or PALM.

Query Match 84.6%; Score 899; DB 12; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.1e-92;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

32 MEKIPVSAFLLVALSNTYIARDTIVPKGAKCDTKDSRPLQPTLSRGWGDOLIWQTYYE 60
 1 MEKIPVSAFLLVALSNTYIARDTIVPKGAKCDTKDSRPLQPTLSRGWGDOLIWQTYYE 60
 92 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 151
 61 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 120

152 DGQYPRIMFVDPSLTVRADITGRYSNRLAYEPADTLIDNMKKALKLTEL 206
 121 DGQYPRIMFVDPSLTVRADITGRYSNRLAYEPADTLIDNMKKALKLTEL 206

61 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 151
 92 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 151
 61 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 120

RESULT 10
 US-10-243-431-28
 Sequence 28, Application US/10243431
 Publication No. US20030138903A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton,Dan
 APPLICANT: Filvaroff,Ellen
 APPLICANT: Goddard,Audrey
 APPLICANT: Grimaldi,J. Christopher
 APPLICANT: Gurney,Austin
 APPLICANT: Smith,Victoria
 APPLICANT: Stephan,Jean-Philippe
 APPLICANT: Watanabe,Colin
 APPLICANT: Wood,William
 APPLICANT: Zhang,Zemin
 APPLICANT: Fong,Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630RLC37
 CURRENT APPLICATION NUMBER: US/10/243,431
 CURRENT FILING DATE: 2002-09-12
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 28
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-243-431-28

Query Match 84.6%; Score 899; DB 12; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.1e-92;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

32 MEKIPVSAFLLVALSNTYIARDTIVPKGAKCDTKDSRPLQPTLSRGWGDOLIWQTYYE 91
 1 MEKIPVSAFLLVALSNTYIARDTIVPKGAKCDTKDSRPLQPTLSRGWGDOLIWQTYYE 91
 92 ALYSKTSNPKLMIHHLDECPHSOALKVFAENKEIQLAEQFVLLNLVETTDKHLSP 151

Qy 152 DGOYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKAKLKLKTEL 206
 Db 121 DGOYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKAKLKLKTEL 175

RESULT 11
 ; Sequence 28, Application US/0245164
 ; Publication No. US20030138904A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Bacon, Dan
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe
 ; APPLICANT: Watson, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P1630RIC76
 ; CURRENT APPLICATION NUMBER: US/10/245,164
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/19942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO: 28
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien

Query Match 84.6%; Score 899; DB 12; Length 175;
 Best Local Similarity 100%; Pred. No. 2.1e-92; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSAILLVALSNTLARDTTVKPAGKDKTDSPRLPQTLSRGNGDQLIWTQTYEE 91
 Db 1 MEKIPVSAILLVALSNTLARDTTVKPAGKDKTDSPRLPQTLRGNGDQLIWTQTYEE 60

Qy 92 ALYKSNTSNKPLMIITHLDECPCPHSQAIIKKVFAENKEIOKLAOFVLLNLVETTKHLSP 151
 Db 61 ALYKSNTSNKPLMIITHLDECPCPHSQAIIKKVFAENKEIOKLAOFVLLNLVETTKHLSP 120

Qy 152 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKAKLKLKTEL 206
 Db 121 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKAKLKLKTEL 175

RESULT 13
 US-10-244-972-28
 ; Sequence 28, Application US/10244972
 ; Publication No. US20030170809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Andre
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe
 ; APPLICANT: Watson, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630RIC75
 ; CURRENT APPLICATION NUMBER: US/10/244,972
 ; CURRENT FILING DATE: 2004-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/073689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/088478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/091358
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/099803
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/106932
 PRIOR FILING DATE: 1998-11-03
 PRIOR APPLICATION NUMBER: 60/115554
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/119342
 PRIOR FILING DATE: 1999-02-09
 PRIOR APPLICATION NUMBER: 60/123957
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123972
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: 60/127372
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/131271
 PRIOR FILING DATE: 1999-04-27
 PRIOR APPLICATION NUMBER: 60/133459
 PRIOR FILING DATE: 1999-05-11
 PRIOR APPLICATION NUMBER: 60/135725
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: 60/135729
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: 60/135750
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: 60/138385
 PRIOR FILING DATE: 1999-06-09
 PRIOR APPLICATION NUMBER: 60/140653
 PRIOR FILING DATE: 1999-06-22
 PRIOR APPLICATION NUMBER: 60/141037
 PRIOR FILING DATE: 1999-06-23
 PRIOR APPLICATION NUMBER: 60/144732
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 60/144758
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 60/144790
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 60/145228
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 60/145698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: 60/146222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: 60/146843
 PRIOR FILING DATE: 1999-08-03
 PRIOR APPLICATION NUMBER: 60/148188
 PRIOR FILING DATE: 1999-08-10
 PRIOR FILING NUMBER: 60/148513
 PRIOR FILING DATE: 1999-08-12
 PRIOR APPLICATION NUMBER: 60/149327
 PRIOR FILING DATE: 1999-08-17
 PRIOR APPLICATION NUMBER: 60/149395
 PRIOR FILING DATE: 1999-08-17
 PRIOR FILING NUMBER: 60/150114
 PRIOR FILING DATE: 1999-08-20
 PRIOR APPLICATION NUMBER: 60/151700
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: 60/151734
 PRIOR FILING DATE: 1999-08-31

Query 84.6% ; Score 899; DB 12; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.1e-92; Mismatches 0; Indels 0; Gaps 0;
 Matches 175; Conservative 0;

Seq ID NO 28
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-244-972-28

Query Match 32 MEKIPUSAFLLIVALSYTLARDTTVKPAGAKDTKOSRPLKLPQTLSRGWGDLINTQTYEE 91
 Db 1 MEKIPUSAFLLIVALSYTLARDTTVKPAGAKDTKOSRPLKLPQTLSRGWGDLINTQTYEE 60
 Query 92 ALYKSSTSNKPLMITHHLDCEPHSQALKVFAENKEIQLAEQFVNLYETTDKHLSP 151
 Db 61 ALYKSSTSNKPLMITHHLDCEPHSQALKVFAENKEIQLAEQFVNLYETTDKHLSP 120

Query 152 DGQQYPRIMFVDPSSLTVRADITGTRYSNRLAYEPAIDLALLDNMKCAKLKTEL 206
 Db 121 DGQQYPRIMFVDPSSLTVRADITGTRYSNRLAYEPAIDLALLDNMKCAKLKTEL 175

RESULT 14
 US-10-197-942-28.
 Sequence 28, Application US/10197942
 Publication No. US20030175882A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watane, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3630R1C1 (US)
 CURRENT APPLICATION NUMBER: US/10/197, 942
 CURRENT FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/073689

PRIOR APPLICATION NUMBER: 60/162506
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: 60/170262
 PRIOR FILING DATE: 1999-12-09
 PRIOR APPLICATION NUMBER: 60/177118
 PRIOR FILING DATE: 2000-01-20
 PRIOR APPLICATION NUMBER: 60/179851
 PRIOR FILING DATE: 2000-02-02
 PRIOR APPLICATION NUMBER: 60/180921
 PRIOR FILING DATE: 2000-02-08
 PRIOR APPLICATION NUMBER: 60/187202
 PRIOR FILING DATE: 2000-03-03
 PRIOR APPLICATION NUMBER: 60/198587
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: 60/199614
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 60/206330
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/206368
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/209832
 PRIOR FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: 60/218371
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/222695
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: 60/229896
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 60/230621
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/232887
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 60/235147
 PRIOR FILING DATE: 2000-09-22
 PRIOR APPLICATION NUMBER: 60/261878
 PRIOR FILING DATE: 2001-01-12
 PRIOR APPLICATION NUMBER: 60/261910
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/261939
 PRIOR APPLICATION NUMBER: 60/262150
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/264395
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 60/266421
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 60/267623
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/274399
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/280982
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/282129
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/282199
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/290589
 PRIOR FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: 09/180997
 PRIOR FILING DATE: 1998-11-19
 PRIOR APPLICATION NUMBER: 09/267213
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 09/380137
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/380138
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 0/403297
 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: 09/423741
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: 09/709238
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 09/802706

PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 09/872035
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 09/924419
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: 09/927796
 PRIOR FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/929404
 PRIOR FILING DATE: 2001-08-13
 PRIOR APPLICATION NUMBER: 09/931836
 PRIOR FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: 09/941992
 PRIOR FILING DATE: 2001-08-28
 PRIOR APPLICATION NUMBER: 09/946374
 PRIOR FILING DATE: 2001-09-04
 PRIOR APPLICATION NUMBER: 10/001054
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 10/081056
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: 10/119480
 PRIOR FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: PCT/US98/18824
 PRIOR FILING DATE: 1998-09-10

Query Match Score 899; DB 12; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.1e-32;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSAFLLVLVALSNTLARDTIVKPGAKKDTKDSREPLKPTLSRGWGDOLIWTOTYEE 91
 Db 1 MEKIPVSAFLLVLVALSNTLARDTIVKPGAKKDTKDSREPLKPTLSRGWGDOLIWTOTYEE 60

Qy 92 ALYKSKTNSKPKLMITHDECPHSQALKKVEAENKEIQKLAQFQLVILNLYETTDKLSP 151
 Db 61 ALYKSKTNSKPKLMITHDECPHSQALKKVEAENKEIQGLAEQFLVILNLYETTDKLSP 120

Qy 152 DGQYVPRIMFDPSLTVRADITGRYSNLAYEPADTLNDMKALKLTEL 206
 Db 121 DGQYVPRIMFDPSLTVRADITGRYSNLAYEPADTLNDMKALKLTEL 175

RESULT 15
 US-10-248-196-28
 Sequence 28, Application US/10238196
 Publication No. US20030186372A1
 GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin
 / APPLICANT: Eaton, Dan
 / APPLICANT: Filavroff, Ellen
 / APPLICANT: Godard, Audrey
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Guiney, Austin
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stephan, Jean-Philippe
 / APPLICANT: Watane, Colin
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / APPLICANT: Fong, Sherman
 / APPLICANT: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3610R1C8
 / CURRENT APPLICATION NUMBER: US/10/238,196
 / CURRENT FILING DATE: 2002-07-18
 / PRIOR APPLICATION NUMBER: 10/197942
 / PRIOR FILING DATE: 2002-07-18
 / PRIOR APPLICATION NUMBER: 60/4059114
 / PRIOR FILING DATE: 1997-09-17
 / PRIOR APPLICATION NUMBER: 60/063046
 / PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-35
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO: 28
LENGTH: 175
TYPE: PRT
ORGANISM: Homo Sapien
US-10-238-196-28

Query Match 84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 32 MEKIPVSAFLILVALSNTLARDTTVKGAKKDTKDSRKLUQTLSPRGWDOLINTOTYEE 91
Db 1 MEKIPVSAFLILVALSNTLARDTTVKGAKKDTKDSRKLUQTLSPRGWDOLINTOTYEE 60
Oy 92 ALYKSNSKPKLMITHLDECPHSQALKVFAENKEIQLAEQFVILLNLYETTDKHLSP 151
Db 61 ALYKSNSKPKLMITHLDECPHSQALKVFAENKEIQLAEQFVILLNLYETTDKHLSP 120
Oy 152 DGQYVPRIMFYDPSLTVRADITGGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
Db 121 DGQYVPRIMFYDPSLTVRADITGGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 175

Search completed: November 26, 2003, 16:01:22
Job time : 32 secs

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PROTEIN - PROTEIN SEARCH, USING SW MODEL

Run on: November 26, 2003, 15:53:44 ; Search time 21. Seconds
(without alignment updates) A15 049 million cell updates / sec

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Perfect score: 1063

1

Scoring case: **Gordon 10 0 Gadax 0 E**

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Minimum DB seq length: 0
Maximum DB seq length: 300000000

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Maximum Match 100%

THE JOURNAL OF CLIMATE

Database : ISSUES-FACULTY-ADMISSIONS / 1 / 1000 / 153 GOURI DASGUPTA

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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1	899	84.6	175	3	US-08-916-576B-2		Sequence 2, Appli
2	899	84.6	175	4	US-09-0247-155-06		Sequence 106, Appli
3	609.5	57.3	170	3	US-08-916-576B-8		Sequence 8, Appli
4	605	56.9	131	4	US-09-247-155-74		Sequence 174, Appli
5	555	52.2	166	3	US-08-916-576B-6		Sequence 6, Appli
6	448	42.1	183	3	US-08-916-576B-7		Sequence 7, Appli
7	222	20.9	172	3	US-08-916-576B-4		Sequence 4, Appli
8	88.5	8.3	118	4	US-09-198-452A-1234		Sequence 1234, Appli
9	81.5	7.7	901	2	US-08-884-881-5		Sequence 5, Appli
10	81.5	7.7	901	3	US-09-258-643-5		Sequence 5, Appli
11	81.5	7.7	968	3	US-08-560-005-7		Sequence 7, Appli
12	81.5	7.7	968	3	US-09-418-840-7		Sequence 7, Appli
13	81.5	7.7	968	4	US-09-969-528-7		Sequence 7, Appli
14	79	7.4	166	4	US-09-198-152A-998		Sequence 998, Appli
15	78	7.3	129	4	US-09-534-638-5		Sequence 5, Appli
16	78	7.3	453	3	US-09-013-881-5		Sequence 5, Appli
17	78	7.3	453	4	US-09-612-473-5		Sequence 5, Appli
18	78	7.3	1160	5	PCT-US92-05401-4		Sequence 4, Appli
19	77	7.2	652	2	US-08-313-185-53		Sequence 53, Appli
20	77	7.2	652	2	US-08-459-499-17		Sequence 17, Appli
21	77	7.2	652	2	US-09-082-614A-53		Sequence 53, Appli
22	77	7.2	1049	4	US-09-107-532A-5966		Sequence 5966, Appli
23	74.5	7.0	2321	4	US-09-023-652-2		Sequence 2, Appli
24	74	7.0	264	3	US-09-053-197A-8		Sequence 8, Appli
25	74	7.0	264	4	US-09-085-761A-8		Sequence 8, Appli
26	73.5	6.9	1049	4	US-09-252-999A-17298		Sequence 17298, Appli
27	73	6.9	1067	4	US-09-107-532A-5148		Sequence 5148, Appli

ALIGNMENTS

```

RESULT 1
US-08-916-576B-2 Application US/08916576B
; Sequence 2, Application US/08916576B
; Patent No. 6171816

; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBNER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 22-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-576B-2

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STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: US
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/916,576B
 FILING DATE: 08/08/1996
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA: US 60/024,347
 APPLICATION NUMBER: 60/024,347
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.05000001
 TELECOMMUNICATION INFORMATION:
 FILING DATE: 23-AUG-1996
 TELEPHONE: (202) 371-2600
 TELEX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-916-576B-8

RESULT 2
 US-08-247-155-106
 Sequence 106, Application US/09247155A
 ; Sequence 106, Application US/09247155A
 ; General Information:
 ; Applicant: Dumas Milne Edwards, Jean-Baptiste
 ; Applicant: Duclert, Aymeric
 ; Applicant: Bougueret, Lydie
 ; Title of Invention: Complementary DNAs
 ; File Reference: GENSET 021A
 ; Current Application Number: US/09/247,155A
 ; Current Filing Date: 1999-02-09
 ; Earlier Application Number: 60/074,121
 ; Earlier Filing Date: 1998-02-09
 ; Earlier Application Number: 60/081,563
 ; Earlier Filing Date: 1998-04-13
 ; Earlier Application Number: 60/096,116
 ; Earlier Filing Date: 1998-06-10
 ; Earlier Application Number: 60/099,273
 ; Earlier Filing Date: 1998-10-04
 ; Number of SEQ ID NOS: 182
 ; Software: Patent. pm
 ; SEQ ID NO 106
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: -20...-1
 US-08-247-155-106

Query Match 84.6%; Score 899; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.6e-95;
 Matches 175; Conservative 0; Gaps 0;
 Qy 32 MEKIPVAFLLVALSVALSVALTARDTIVKGAKKDTDSRPLPOTLSRGWQDQLIWTQTYEE 91
 Db 1 MEKIPVAFLLVALSVALSVALTARDTIVKGAKKDTDSRPLPOTLSRGWQDQLIWTQTYEE 60

RESULT 4
 US-09-247-155-174
 Sequence 174, Application US/09247155A
 ; Sequence 174, Application US/09247155A
 ; General Information:
 ; Applicant: Dum Milne Edwards, Jean-Baptiste
 ; Applicant: Duclert, Aymeric
 ; Applicant: Bougueret, Lydie
 ; Title of Invention: Complementary DNAs
 ; File Reference: GENSET 021A
 ; Current Application Number: US/09/247,155A
 ; Current Filing Date: 1999-02-09
 ; Earlier Application Number: 60/074,121
 ; Earlier Filing Date: 1998-02-09
 ; Earlier Application Number: 60/081,563
 ; Earlier Filing Date: 1998-04-13
 ; Earlier Application Number: 60/096,116
 ; Earlier Filing Date: 1998-08-10
 ; Earlier Application Number: 60/099,273
 ; Earlier Filing Date: 1998-10-04
 ; Number of SEQ ID NOS: 182
 ; Software: Patent.pm
 ; SEQ ID NO 174

RESULT 3
 US-08-916-576B-8
 Sequence 8, Application US/08916576B
 ; General Information:
 ; Applicant: YU, GUO-JIANG
 ; Applicant: DILLON, PATRICK J.
 ; Applicant: EBNER, REINHARD
 ; Applicant: ENDRESS, GREGORY A.
 ; Title of Invention: NOVEL HUMAN GROWTH FACTORS
 ; Number of Sequences: 45
 ; Correspondence Address:
 ADDRESSEER: STURNE, KESSLER, GOLDSTEIN & FOX, P. I., L.C.
 ; Software: Patent.pm

LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SIGNAL
; LOCATION: -20..-1
; NAME/KEY: UNSURE
; LOCATION: 40,41,43,60,70,76,82,86,105,107
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
; US-09-247-155-174

Query Match Score 605; DB 4; Length 131;
Best Local Similarity 92.9%; Pred. No. 7.2e-62;
Matches 117; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 32 MEKIPVSAILLIVALSYTLARDTTVKGAKKDTSRPLQPOTLSRGWDOLIWOTYEE 91
Db 1 MEKIPVSAILLIVALSYTLARDTTVKGAKKDTSRPLQPOTLSRGWDOLIWOTYEX 60

Qy 92 ALYKSKTSNPKPLMIHHLDECPSQALKXQFAENKXIQKLAXQFTXNLVETTDGHSLP 151
Db 61 XLKXKTSNPKPLMIHHLDECPSQALKXQFAENKXIQKLAXQFTXNLVETTDGHSLP 120

Qy 152 DGQYVP 157
Db 121 DGQYXP 126

RESULT 5
US-08-916-576B-6
; Sequence 6, Application US/08916576B
; Patent No. 6171816

GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBNER, REINHARD
; APPLICANT: ENDRASS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.1, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-916-576B-7

Query Match Score 448; DB 3; Length 183;
Best Local Similarity 49.4%; Pred. No. 1.4e-43;
Matches 88; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

Qy 39 AFLILVALSYTLARDTTVKGAKKDTSRPLQPOTLSRGWDOLIWOTYEE 89
Db 6 SLVCLVLLCSALGAVLCKPKHQACTTDTDQBPAPIKTKGLCUDREWGBSLEWQTY 65

Qy 90 EEALEYKSSTSNSKPKLMIIHHLDECPSQALKXQFAENKEIQLA EQFVLLNLIVETTDKH 148

RESULT 7
US-08-916-576B-4
Sequence 4, Application US/08916576B
GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
APPLICANT: EBNER, REINHARD D.
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0500001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-576B-4

Query Match 20.9%; Score 222; DB 3; Length 172;
Best Local Similarity 34.2%; Pred. No. 1.4e-17;
Matches 54; Conservative 26; N mismatches 56; Indels 22; Gaps 3;

Qy 66 DSRPKLPT-----LSRGWGDQLIWTOYEALIYSKTSNPKLMITI 106
Db 2 ETRPRIGATCLGFSFLLLVSSDGHNLGLKGFDHINW-RTLEDGKKEAAASGIPMVI 60

Qy 107 HHLDECPHSQALKVFAENKEIQLAEQFYLLN--VYETTDKHLSPDCGYPRIMFVDP 164
Db 61 IHKSWGACKALKPKFAESTEISEUSHNFVNLDDEEEFKDDEFSPDGYPRILFLDP 120

Qy 165 SLTVRADITGRYSNRLYAYEPADTALLDNMKKALKL 202
Db 121 SGKVHEPINENGNPSPKYFYVSAEQVQGMKAQERL 158

RESULT 8
US-09-198-452A-1234
Sequence 1234, Application US/09198452A

; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Giffrais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO: 1234
; LENGTH: 118
; TYPE: PROTEIN
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-1234
Query Match 8.3%; Score 88.5; DB 4; Length 118;
Best Local Similarity 8.6%; Pred. No. 0.018;
Matches 33; Conservative 29; N mismatches 45; Indels 27; Gaps 5;
Qy 29 RVMEKIPVSATILIVLVASITYLARDDTYKPGAKKDKDSRPGKDQLINTQT 88
Db 9 RCSLKOKLVATLIL--LSSL--PTEAAENRDS-----DSIRWHLD 46
Qy 89 YEEALYKSKTSNPKLMITHLDBC--PHSQALKVFAENKEIQLAEQFYLLNVEYETD 146
Db 47 KHLSPDGQXVPRIM 160
Qy 147 KHLSPDGQXVPRIM 160
Db 104 KHRPQLKTFSKIL 117
RESULT 9
US-08-854-681-5
Sequence 5, Application US/08884681
Patent No. 5953238
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neill C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,681
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
FILE NUMBER: PF-0334 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 901 amino acids
TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1420920
 US-08-884-681-5

Query Match 7.7%; Score 81.5; DB 3; Length 901;
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Query Match 7.7%; Score 81.5; DB 3; Length 901;
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;

Query Match 7.7%; Score 81.5; DB 3; Length 901;
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 45; Conservative 45; Mismatches 32; Indels 67; Gaps 13;

Query 55 TVKPGAKKDKDSRPK-LPQTLSRGWGQJLWTOYEAL-YKS---KTS-NKPLMII 106
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Db 476 TYKYDSKTDWRDSSGCRVP-----AWCDRILWRGTNVNQLNYRSHMELKTSDHKEPSAL 530
 Query 107 HHL----DECPSQALKVPAENKEIQLAE-----QTVLLNLVYETTDK- 147
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Db 531 FHIGVKVDE---RRYRKVFEDSVRIMDRMENDFLPSLESRREFEVENVKFRLQKGK 586
 Query 148 -HLSPDGQ----YVPRIM-----FVDPSLTVRADITGRYSNLYAYE 184
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Db 587 FQISNNCQVPCHFSF1PKLNDSQYCKPWLRRAEPFEGYLEPNETV--DIS-----LDVVY 638
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Query 185 PADTALLDN 194
 Best Local Similarity 23.7%; Pred. No. 2.3;
 Mismatches 32; Indels 67; Gaps 13;

Db 639 SKDSVTILNS 648

RESULT 11
 US-09-560-005-7
 Sequence 7, Application US/08560005
 Patent No. 6001354

GENERAL INFORMATION:
 APPLICANT: Pot, David A.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Williams, Lewis T.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Jefferson, Anne Bennett
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Majorus, Phillip W.
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: Grb2 Associating Protein and Nucleic
 ACIDS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/560,005
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 2307K-0624000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 968 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..968
 OTHER INFORMATION: /note= "ocrl"

Query Match 7.7%; Score 81.5; DB 3; Length 968;
 Best Local Similarity 23.7%; Pred. No. 2.6;
 Mismatches 32; Indels 67; Gaps 13;

US-08-560-005-7

STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1420920

QY 55 TVKPGAKDKTDKDSRPK-LPOTLSRGWGDQLIWTQTYEAL-YKS---KTS-NKPLMII 106
 Db 551 TYKDKSDTKDRWSSGKCRVP----AWCDRILWRGTNQNLYRSHMLKTSDBHKPVSAL 605
 QY 107 HHL----DECPHSQALKRKVFAENKEQLRKE-QKLAE-----QFVLNLVYETTDK-- 147
 Db 606 FHIGVKVDE----RRYRKVFEDSVRIMDRMENDFLSLESLSRREFVENVKFRQLQKGK 661
 QY 148 -HLSPDGQ-----YVPRIM-----FVDPSLTYRADITGRYSNRLYAYE 184
 Db 662 FQISNNNGQPCHFSFIPKLNDSQYCKDWLRASPPEGYLEPNETV--DLS-----LDVYV 713
 QY 185 PAPTALLDN 194
 Db 714 SKSDSTLNS 723

RESULT 12
 US-09-418-540-7
 Sequence 7, Application US/09418540
 Patent No. 6296648
 GENERAL INFORMATION:
 APPLICANT: Pot, David A.
 APPLICANT: Williams, Lewis T.
 APPLICANT: Jefferson, Anne Bennett
 APPLICANT: Majorus, Philip W.
 TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic Acid Encoding Therefor
 TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic Acid Encoding Therefor
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/418,540
 FILING DATE: 14-OCT-1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/560,005
 FILING DATE: 17-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 TELEPHONE: 415-326-2422
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 968 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..968
 OTHER INFORMATION: /note= "ocr1"
 US-09-418-540-7

Query Match 7.7%; Score 81.5; DB 4; Length 968;
 Best Local Similarity 23.7%; Pred. No. 2.6;
 Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;
 OTHER DESCRIPTION: SEQ ID NO: 7:
 US-09-965-528-7

QY 55 TVKPGAKDKTDKDSRPK-LPOTLSRGWGDQLIWTQTYEAL-YKS---KTS-NKPLMII 106
 Db 551 TYKDKSDTKDRWSSGKCRVP----AWCDRILWRGTNQNLYRSHMLKTSDBHKPVSAL 605
 QY 107 HHL----DECPHSQALKRKVFAENKEQLRKE-QKLAE-----QFVLNLVYETTDK-- 147
 Db 606 FHIGVKVDE----RRYRKVFEDSVRIMDRMENDFLSLESLSRREFVENVKFRQLQKGK 661
 QY 148 -HLSPDGQ-----YVPRIM-----FVDPSLTYRADITGRYSNRLYAYE 184
 Db 662 FQISNNNGQPCHFSFIPKLNDSQYCKDWLRASPPEGYLEPNETV--DLS-----LDVYV 713
 QY 185 PAPTALLDN 194
 Db 714 SKSDSTLNS 723

RESULT 13
 US-09-965-528-7
 Sequence 7, Application US/0996528
 Patent No. 6472197
 GENERAL INFORMATION:
 APPLICANT: Pot, David A.
 APPLICANT: Williams, Lewis T.
 APPLICANT: Jefferson, Anne Bennett
 APPLICANT: Majorus, Philip W.
 TITLE OF INVENTION: No. 6472197el Grb2 Associating Protein and Nucleic Acid Encoding Therefor
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/969,528
 FILING DATE: 01-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/560,005
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 968 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..968
 OTHER INFORMATION: /note= "ocr1"
 OTHER DESCRIPTION: SEQ ID NO: 7:
 US-09-965-528-7

Query Match 7.7%; Score 81.5; DB 4; Length 968;
 Best Local Similarity 23.7%; Pred. No. 2.6;
 Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;
 OTHER DESCRIPTION: SEQ ID NO: 7:
 US-09-965-528-7

QY 55 TVKPGAKDKTDKDSRPK-LPOTLSRGWGDQLIWTQTYEAL-YKS---KTS-NKPLMII 106

Db 551 TYKDSKTDRWDSGGKCRVP-----AWCDRILMRGTVNQLNVRSHMLIKTSDHKPVSAL 605
 Qy 107 HHL----DECPHSQALRKVFAENKEIQKLAE-----QFYILLNLYYETTDK-- 147
 Db 606 PHICGVKVDE---RRPKVFEDSVRMIDRMENDFLPSLELSREFTFENVKFRQLQKGK 661
 Qy 148 -HLSPDGQ-----VPRIM-----FVDPSLTVRADITGRYSNRLYAYE 184
 Db 662 PQISNNNGOPCPHSFIPLKNDSOYCKPMRAEBEGYLEPNEYV-DIS-----LIVVV 713
 Qy 185 PADTALLDN 194
 Db 714 SKDSVTLNS 723

RESULT 14

US-09-198-452A-998

; Sequence 998, Application US/09198452A

; Patent No. 6552294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments of title of invention: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION:

; FILE REFERENCE: 9710-003-999

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO: 998

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-998

Query Match Score 79; DB 4; Length 166;
 Best Local Similarity 24.2%; Prod. No. 0.37;
 Matches 43; Conservative 27; Mismatches 70; Indels 38; Gaps 9;

Qy 40 FLLVASYTLARDTIVPGARKDTKDSRPLQPTLRSRGWDQLMWQTYBEALYKSCTS 99
 Db 10 FCRLSADFTLLCCT-KTCFWRNLLQQTTRPIAAANLQ-----W-ESYAEALEHSKQD 58
 Qy 100 NKPL-MIHHHLDECPSQALKKVFIAENKEIQKLAEEQFYILLNLYYETTDK 147
 Db 59 HRPCLFTGSPDCMWC1KMQDQIQLQSEFHKFAG-VHLLRNEVDPQKHNHQPEQRQK 116
 Qy 148 HLSPDGQ-----VPRIMFVDPSLTVRADITGRYSNRLYAYEADTALLDNMKKALKL 201
 Db 117 NOELKAGQKVTFGPPELFIDAE-----GRQLARN-GFEGGGAAAVSKVKSALKL 165

RESULT 15

US-09-534-638-5

; Sequence 5, Application US/09534638

; Patent No. 6320038

; GENERAL INFORMATION:

; APPLICANT: Panula, Pertti A.J.

; APPLICANT: Brandt, Annika

; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof

; TITLE OF INVENTION: for therapy and diagnosis

; FILE REFERENCE: 2530-104

; CURRENT FILING DATE: 2000-01-27

; EARLIER APPLICATION NUMBER: 09/365755

; EARLIER FILING DATE: 1999-08-03

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 5

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Mouse

US-09-534-638-5

Query Match Score 7.3%; DB 4;
 Best Local Similarity 22.9%; Prod. No. 0.34;
 Matches 16; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
 Qy 44 VALSYTLARDTIVPGAKDKDTKDSRPLQPTLRSRGWDQLMWQTYBEALYKSCTS 103
 Db 3 IAFYILLTCNSNTSPSSRNSTQSGSPOAVVDSDRWEDTVAVLLOKCLLSFPSSQFSM 62
 Qy 104 MIHHHLDECPL 113
 Db 63 TPVSLQSQP 72

Search completed: November 26, 2003, 15:56:59

Job time : 22 sec

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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - nucleic search, using frame_Plus_P2n model
 Run on: November 30, 2003, 02:24:26 ; Search time 64 Seconds
 (without alignments)
 1420.702 Million cell updates/sec
 Title: US-09-674-266A-181
 Perfect Score: 1063
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 Scoring table: BLOSUM62
 Xgapext 10.0 , Ygapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0
 Searched: 569978 seqs, 220691566 residues
 Total number of hits satisfying chosen parameters: 1139956
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Command line parameters:
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 -LOOPEXT=6 -UNITS=5nts -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR SCORE-PCT =-THR MAX=-100 -THR MIN=-15
 -MODE=LOCAL -OUTFMT=pto -NOR=ext -HEAPSIZE=800 -MINLEN=0 -MAXLEN=2000000000
 -NO MMAP -USER=US09674266 @CCN_1.152@runat:26112003.152/49.15781 -NCPU=6 -ICPU=3
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAP=0 -WAIT -DSBLOCK=100 -LONGLOG
 -FGAPEXT=7 -YGAPOP=10 -XGAPEXT=0.5 -DEPLEX=7

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 2: /cgn2_6/podata/1/ina/5B COMB seq: *
 3: /cgn2_6/podata/1/ina/6A COMB seq: *
 4: /cgn2_6/podata/1/ina/6B COMB seq: *
 5: /cgn2_6/podata/1/ina/PCUTS COMB seq: *
 6: /cgn2_6/podata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991	93.2	875	3	Sequence 1, Appli
2	961	90.4	1689	4	Sequence 0-247-15-61
3	914	86.0	940	4	Sequence 0-247-15-149
4	856.5	80.6	793	3	Sequence 0-940-384-78
5	856.5	80.6	793	4	Sequence 0-9-123-912-78
6	856.5	80.6	793	4	Sequence 0-9-643-59-78
7	856.5	80.6	793	4	Sequence 0-0-480-88A-78
8	856.5	80.6	793	4	Sequence 0-0-542-615A-78
9	856.5	80.6	793	4	Sequence 0-0-606-421B-78
10	683	64.3	401	3	Sequence 0-9-221-298-32
11	642	60.4	386	3	Sequence 0-8-916-576B-35
12	631	59.4	404	4	Sequence 0-9-643-59-782

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	916-576B-1	Sequence 1, Application US/08916576B			
2	6171816	Patent No. 6171816			
3	YU, GUO-LIANG	Applicant: YU, GUO-LIANG			
4	DILLON, PATRICK J.	Applicant: DILLON, PATRICK J.			
5	ERNER, REINHARD	Applicant: ERNER, REINHARD			
6	ENDRESS, GREGORY A.	Applicant: ENDRESS, GREGORY A.			
7	GENERAL INFORMATION:				
8	TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS				
9	NUMBER OF SEQUENCES: 45				
10	CORRESPONDENCE ADDRESS:				
11	ADDRESSEE: STEERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.				
12	STREET: 1100 NEW YORK AVENUE, SUITE 600				
13	CITY: WASHINGTON				
14	STATE: DC				
15	COUNTRY: US				
16	ZIP: 20005-934				
17	COMPUTER READABLE FORM:				
18	MEDIUM TYPE: Floppy disk				
19	COMPUTER: IBM PC compatible				
20	OPERATING SYSTEM: PC-DOS/MS-DOS				
21	SOFTWARE: Patentin Release #1.0, Version #1.3.0				
22	APPLICATION NUMBER: US/08/916,576B				
23	CURRENT APPLICATION DATA:				
24	FILING DATE:				
25	CLASSIFICATION: 536				
26	PRIOR APPLICATION DATA:				
27	APPLICATION NUMBER: US 60/024,347				
28	FILING DATE: 23-AUG-1996				
29	ATTORNEY/AGENT INFORMATION:				
30	NAME: STEFFE, ERIC K.				
31	REGISTRATION NUMBER: 36,688				
32	REFERENCE/DOCKET NUMBER: 1488.0500001				
33	TELEPHONE: (202) 371-2600				

QY 132 AlaGluGlnPheValLeuAsnLeuValTyrGlutThrThrAspLysHisLeuSerPro 151
 Db 351 GCAGCCAGTTGTCTCAATGTTATTGAAACACTGAAACCTTTCCT 410

QY 152 AspGlyGlnIrrvalProArgIleMetPheValAspProSerLeuThrValArgAlaAsp 171
 Db 411 GATGCCAGATGTCGCCAGATTATGTTGACCATCTCTGACAGTTAGGCCGAT 470

QY 172 LleIrrgIArgTyserAsnArgLeuTyralaTygluProAlaAspThrAlaIeuLeu 191
 Db 471 ATCACTGGAGATATTCAAATCCTGCTCATGAACTGCAGATACTGGTGTG 530

QY 192 LeuAspAsnMetLysBAlaLeuLysLeuLeuLysLeuLysLeuLysLeuLysLeu 206
 Db 531 CTTGAGACATGAGAAGCTCAAGTGTGAGAATTTG 575

RESULT 3
 US-09-247-155-149
 ; Sequence 149, Application US/09247155A
 ; Patent No. 6312922.

; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards , Jean-Baptiste
 ; APPLICANT: Duclert, Aymeric
 ; APPLICANT: Bouguere, Lydie
 ; TITLE OF INVENTION: Complementary DNAs
 ; FILE REFERENCE: GENSET 021A
 ; CURRENT APPLICATION NUMBER: US/09/247,155A
 ; CURRENT FILING DATE: 1999-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,121
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/081,563
 ; EARLIER FILING DATE: 1998-04-13
 ; EARLIER APPLICATION NUMBER: 60/096,116
 ; EARLIER FILING DATE: 1998-08-10
 ; EARLIER APPLICATION NUMBER: 60/099,273
 ; EARLIER FILING DATE: 1998-10-04
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: Patent .pm
 ; SEQ ID NO: 149
 ; LENGTH: 940
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 177..569
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 177..236
 ; OTHER INFORMATION: Von Hejne matrix
 ; OTHER INFORMATION: score 11.199999092651
 ; OTHER INFORMATION: seq AFILVLAISYTLARD
 ; FEATURE:
 ; NAME/KEY: polyA_site
 ; LOCATION: 931..939
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 482
 ; OTHER INFORMATION: n=a, g, c or t

US-09-247-155-149

Alignment Scores:
 Pred. No.: 5.15e-107
 Score: 914.00
 Percent Similarity: 90.82%
 Best Local Similarity: 90.82%
 Query Match: 85.98%
 DB: 4

Length: 940
 Matches: 188
 Conservative: 0
 Mismatches: 12
 Indels: 8
 Gaps: 1

QY 21 GlngIArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaAlphe 40
 Db 162 CAAGC-----AGAGTTGCCGTGGAAAATANTCCAGTGTGGCACATC 203

QY 41 LeuLeuLeuValAlaLeuSerTyrThrIeuAlaArgAspThrThrValLysProGlyAla 60
 Db 204 TTGTCCTGTCGCCCTCTCAACTTGCCRAGATAACAGTCAAACCTGGAGCC 263

QY 61 LysIysAspThrLysAspSerAspProLysLeuProGlnThrIeuSerArgGlyIrrGly 80
 Db 264 AAAAGGACAAGGAACCTGACGCCAACACTGCCAGACCCCTCCAGGGTGGGGT 323

QY 81 AspGlnLeuIleIrrpHsGlnThrGlnThrIrrgIgluLalaLeuIrrlysSerLysThrSerAsn 100
 Db 324 GACCAACTCATCGACACCARAGTATGARAARCTPATWTAATCCAARACAGCACAC 383

QY 101 LysProLeuMetIleIleIrrHisIleuLysPGLucySProHisSerGlnAlaLysLysLys 120
 Db 384 ARACCCTTGATGATTGATCATCATTCGATGADTTGATGADTTGATGADTTGATC 443

QY 121 ValIrrHeLaGluAsnLysGluIleGlnLysLeuIrrAlaGluGlnPheValLeuAsnLeu 140
 Db 444 KTGTGTTGCTGAAATAAAATAATCAGAAATTCGAAATTCGCAACATCAAGCTTAAAAA 503

QY 141 ValIrrGluIrrThrIrrAspLysIleuSerProGlyGlnIrrVal-ProArgIleIle 160
 Db 504 GTRPATGAAACACTGACAACACCTTCTCCCTGATGCCAATAATKTCCCAGGATT 563

QY 160 tPheValAspProSerLeuThrValArgAlaAspIrrLysGlyArgTyrSerAnArgLe 180
 Db 564 GTRTGTGACCCATCTCTGACAGTTAGGCCGATACACTGGAGATATTCAGTCAGTCT 623

QY 180 utrYAlaTyrGluProAlaAspTrAlaLeuLeuLysPAsmIrrLysBAlaLeuLys 200
 Db 624 CTATGCTTGAAGCTGAGATAAGCTGAGATAAGCTGAGAAAGCTCTCAA 683

QY 200 sIleLeuLysThrCluLeu 206
 Db 684 GTRGCTGAAAGACTGAAATTG 702

RESULT 4
 US-09-090-984-78
 ; Sequence 78, Application US/09040984
 ; Patent No. 6210883

; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Wang, Tonglong
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
 ; TITLE OF INVENTION: OF LUNG CANCER
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastBQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/040,984
 ; FILING DATE: 18-MAR-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Makin, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.456
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-622-4900

QY 1 ArgLeuSerCysAlaGlyIrrIrrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Db 103 AGACTCAGCTGTCGAGCAGCTCAAGAGCTTAGCCGAGACTCACA 161

TELEFAX: 206-282-6031
 TELEX:
 INFORMATION FOR SEQ ID NO: 78.
 SEQUENCE CHARACTERISTICS:
 LENGTH: 793 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-040-984-78

Alignment Scores:
 Pred No.: 8 5.7e-100 Length: 793
 Score: 856.50 Matches: 177
 Percent Similarity: 94.74% Conservative: 3
 Best Local Similarity: 93.16% Mismatches: 9
 Query Match: 80.57% Inels: 3
 DB: 3 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-040-984-78 (1-793)

Qy 14 HisProSerArgProlLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33
 Db 2 CATECTAGCCGCACTCACACAGGGCGGTGGTGGAAATTCAGGTTGCCATGGAG 61

Qy 34 LysIleProValSerAlaPheLeuLeuLeuValAlaSerThrLeuAlaArgAsp 53
 Db 62 AAATTTCAGTGTCAGCATCTGCTCCCTACACTCTGSCCAGAGAT 121

Qy 54 ThrThrValLysProGlyAlaLysAspThrLysAspSerArgProLysLeuProGln 73
 Db 122 ACCACAGTCAAACCTGGGCCAAAAGGACACAAGGACTCTGACCAAACTGCCDAG 181

Qy 74 ThrIleSerArgGlyTrpGlyArgGlnLeuIleTrpPheGlnThrTyrgluGluIaleu 93
 Db 182 ACCCTCTCCAGTAGGTGGGTGACCATGATGAGCTCTCA 241

Qy 94 TyrLyserLysThrSerAsnLysProLeuMetIleIleHisIleLeuAspGluCysPro 113
 Db 242 TATAATCCAAGAACAAACCCCTGATGATTATCATCACTTGATGATGTGCCA 301

Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
 Db 302 CACAGTCAGCTTAAGAAAGTCTGCTGAATAATCAGAAATGGCAAG 361

Qy 134 GlnPheValLeuAsnLeuValTyrgluThrThrAspLysLeuSerProAspGly 153
 Db 362 CAGTTGCTCTCAATTGGTTATGAAACACTGCAAACCTTCTCTGTGAGC 421

Qy 154 GlntYrValProArgIleMetPheValAspProSerIleThrValArgAlaAspIleThr 173
 Db 422 CAGPATGTCCCAGGATPATGTTGTTAACCATCTCGACACTTGAAGCCATATCTG 480

Qy 174 GlyArgTrpSerAsnArgLeuTyrylProAlaAspThrAlaLeuLeuLeuAsp 193
 Db 481 GGAGATATTCAACCGCTCTAGCTTACAAACT-GCAGATACGCTCTGCTGCTGCA 539

Qy 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203
 Db 540 CAT---GAAAAAGCTCAAGTGTCTAAA 566'

RESULT 5
 US-09-123-912-78
 ; Sequence 78, Application US/09123912A
 ; Patent No. 6312695
 ; GENERAL INFORMATION;
 ; APPLICANT: Wang Tongtong
 ; FILE REFERENCE: 2,0121-455C1
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
 ; CURRENT APPLICATION NUMBER: US/09/123, 912A
 ; CURRENT FILING DATE: 1998-07-27
 ; PRIOR APPLICATION NUMBER: US/09/040, 802
 ; PRIOR FILING DATE: 1998-03-18

; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 78
 ; LENGTH: 793
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: modified_base
 ; LOCATION: (1309)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (492)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (563)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (657)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (660)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (703)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (708)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (710)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (711)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (732)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (740)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (748)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (758)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (762)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; NAME/KEY: modified_base
 ; LOCATION: (787)
 ; OTHER INFORMATION: Where n is a, c, g or t
 ; US-09-123-912-78

Alignment Scores:
 Pred. No.: 8.57e-100 Length: 793
 Score: 856.50 Matches: 177
 Percent Similarity: 94.74% Conservative: 3
 Best Local Similarity: 93.16% Mismatches: 9
 Query Match: 80.57% Indels: 3
 DB: 4 Gaps: 1
 US-09-674-266A-181 (1-206) x US-09-123-912-78 (1-793)

Qy 14 HisProSerArgLysLeuIleGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33
 Db 2 CATTAGCCGGGACTCACACAGGAGGTGGTGGAAATCAGAGTGTGCCATGAG 61
 Qy 34 LysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerThrLeuAlaArgAsp 53

DB: 62 AAAATTCCAGTGTCAAGGATTCCTGGCTCCTTGCCCCCTCTACACTCTGCCAGAGAT 121
 Qy 54 ThrThrValLeuProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
 DB: 122 ACCACAGTCAACCTGGCCAAARGACCAAAAGACTCTGACCACAACTGCCAG 181
 Qy 74 ThrLeuSerArgGlyTrpGlyAspGlnLeuIlePheGlnThrTrgGluAlaLeu 93
 DB: 182 ACCCTCCCAGGGTGGGACCAACTCATCTGAACTAGACATAAGAGCTTA 241
 Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisIleLeu 113
 DB: 242 TATAAATCCAGACAGCAAAACCTTGATGATTCTCATCTGGATGAGTCCCCA 301
 Qy 114 HisSerGlnAlaLeuLysLysValValPheAlaGluAlaLysGluIleGlnLysLeuAlaGlu 133
 DB: 302 CACAGTCAAGCTTTAAAAGAARGTGTGCTGAAATAAGAAATCCGAATTGGCAG 361
 Qy 134 GlnPheValLeuLeuLeuValValPheAlaGluAspLeuSerProAspGly 153
 DB: 362 CAGTTGTCCTCTCATCTGGTTAGAAACACTGACAACAACTTCCTCGATGCC 421
 Qy 154 GluTyrValProArgLeuMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
 DB: 422 CAGTATG-CCCAAGGATTATCTTGTTGACCCATCTGCACAGTGAACCGGATATCCTG 480
 Qy 174 GLYATGTYRSerAsnArgLeuTyrrAlaTyrrGluProAlaAspThrAlaLeuLeuAsp 193
 DB: 481 GGAAAGTTATTCNAACCGTCCTATGCTTAACTGCAGATACTGCTGCTTGACA 539
 Qy 194 AsnMetLysLysAlaLeuLysLeuLysLys 203
 DB: 540 CAT---GAAAAGCTCAACTGGTCAAATGGTCAA 566

RESULT 6
 US-09-643-597-78
 ; Sequence 78, Application US/09643597
 ; Patent No. 6426072.
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeall, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121455C1.
 ; CURRENT APPLICATION NUMBER: US/09/643,597
 ; CURRENT FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 369
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 78
 ; LENGTH: 793
 ; TYPE: DNA
 ; FEATURE: misc_feature
 ; LOCATION: (1)...(793)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-643-597-78
 Alignment Scores:
 Pred. No.: 8.57e-100 Length: 793
 Score: 856.50 Matches: 177
 Percent Similarity: 94.74% Conservative: 3
 Best Local Similarity: 93.16% Mismatches: 9
 Query Match: 80.57% Indels: 3

DB: 14 HisProSerArgArgLeuThrGlnGlyArgLysSerArgValAlaMetGlu 33
 Qy 14 HisProSerArgArgLeuThrGlnGlyArgLysSerArgValAlaMetGlu 33
 DB: 2 CATCTTAGCCGCGACTCACACAGGCCAGTGGTGAAGTGCATGGAG 61
 Qy 34 LysLysProValSerAlaTheLeuIleLeuValAlaLeuSerTyrrThrLeuAlaArgAsp 53
 DB: 62 AAATTCCAGTGTGACATCTCTCTCTGTCACCTGGCAGATGGAGAT 121
 Qy 54 ThrThrValLeuProGlyAlaLysAspThrLysAspProLysLeuProGln 73
 DB: 122 ACCCTCTCCAGGGTGGGACCAACTCATCTGGACTGAGCTCPA 241
 Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisIleLeu 113
 DB: 182 ACCCTCTCCAGGGTGGGACCAACTCATCTGGACTGAGCTCPA 241
 Qy 74 ThreLeuSerArgGlyTTPGlyAspGlnLeuIlePheAlaGluAlaLeu 93
 DB: 242 TATAAATCCAGACAGCAAAACCTTGATGATTCTCATCTGGATGAGTCCCCA 301
 Qy 114 HisSerGlnAlaLeuLysLysValValPheAlaGluAlaLysLeuAlaGlu 133
 DB: 302 CACAGTCAAGCTTTAAAAGAARGTGTGCTGAAATAAGAAATCCGAATTGGCAG 361
 Qy 134 GlnPheValLeuLeuLeuValValPheAlaGluAlaAspIleThr 173
 DB: 362 CACACTCNAGCTTAAAGAAAGTGTGCTGAAATAAGAAATCCGAATTGGCAG 361
 Qy 154 GluTyrValProArgLeuMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
 DB: 422 CAGTATG-CCCAAGGATTATCTTGTTGACCCATCTGCACAGTGAACCGGATATCCTG 480
 Qy 174 GLYATGTYRSerAsnArgLeuTyrrAlaTyrrGluProAlaAspThrAlaLeuLeuAsp 193
 DB: 481 GGAAAGTTATTCNAACCGTCCTATGCTTAACTGCAGATACTGCTGCTTGACA 539
 Qy 194 AsnMetLysLysAlaLeuLysLeuLysLys 203
 DB: 540 CAT---GAAAAGCTCAACTGGTCAAATGGTCAA 566

RESULT 7
 US-09-480-884A-78
 ; Sequence 78, Application US/09480884A
 ; Patent No. 6482397
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeall, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121455C6.
 ; CURRENT APPLICATION NUMBER: US/09/480,884A
 ; CURRENT FILING DATE: 2001-08-27
 ; NUMBER OF SEQ ID NOS: 330
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 78
 ; LENGTH: 793
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(793)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-480-884A-78
 Alignment Scores:
 Pred. No.: 8.57e-100 Length: 793
 Score: 94.74% Matches: 177
 Percent Similarity: 93.16% Conservative: 3
 Best Local Similarity: 93.16% Mismatches: 9
 Query Match: 80.57% Indels: 3

OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-78

Percent Similarity: 94.74%
Best Local Similarity: 93.16%
Query Match: 80.57%
DB: 4

Score: 856.50
Percent Similarity: 94.74%
Best Local Similarity: 93.16%
Query Match: 80.57%
DB: 1

US-09-674-266A-181 (1-206) x US-09-480-884A-78 (1-793)

Qy 14 HisProSerArgArgLeuThrGlnGlyArgTPValArgLysSerArgValAlaMetGlu 33
Db 2 CATCTAGGCCGGAATCACAAGCACGTGGTGGAAATCCAGTTGCATGGAG 61

34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrrhIleAlaArgAsp 53
Db 62 AAAATTCCAGTGTGCACTCTGCTCTGACATCTGGCTACTCTGGCAGAGAT 121

54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
Db 122 ACCAGTCATAACCTGAGCCAAlAGGACACAAGGACAACTGCCAACCTGGCCAG 181

74 ThrIleSerArgGlyLysTgClyAspGlnLeuIlePheGlnThrYgluGluAlaLeu 93
Db 182 ACCCTCTCCAGAGSTGGGTGCAACTCATCGAGCTCAGACATAAGAAGCTTA 241

94 TyrIysSerLysThrSerAsnLysProLeuMetIleLeuLeuAspLysGlu 113
Db 242 TATAATCCAGACAGGACACRAACCCTGATGTTATCATCTGATGTTGCCC 301

114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
Db 302 CACAGTCAGCTTAAAGAAAGTGTGAAATAGAAATCCGAAATGGCAG 361

134 GlnPheValLeuAsnLeuValTYgluThrThrAspLysHisIleSerProAspGly 153
Db 362 CAGTTGCTCTCCATCTGGTTATGAAACAACTGACAACCTTCTCTGATGCC 421

154 GluTyValProArgIleMetPheValAspProSerLeuThrGlnGlyAsp 173
Db 422 CAGTAGT-CCCAGATTATGTTGACCCATCTCTGACAGTTGAAAGCGATCTG 480

174 GlyArgTyrSerAsnArgLeuTyrrAlaTyrrGluProLysAspThrAlaLeuLeuAsp 193
Db 481 GGAAAGATATCNAACCGTCCTATGCTTACAACT-GCAGATAGCCTCTGCTTACACA 539

194 AsnMetLysLysAlaLeuLysLysLeuLys 203
Db 540 CAT---GAAAAGCTCTCAAGTGTGCTCNAAA 566

RESULT 8
US-09-542-615A-78
; Sequence 78 , Application US/09542615A
; Patent No. 651856
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121-455C8
; CURRENT APPLICATION NUMBER: US/09/542, 615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 78
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; LOCATION: (1) ... (793)

OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-78

Alignment Scores:
Pred. No.: 8.57e-100
Score: 956.50
Percent Similarity: 94.74%
Best Local Similarity: 93.16%
Query Match: 80.57%
DB: 4

Length: 793
Matches: 177
Conservative: 3
Mismatches: 9
Indels: 3
Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-78 (1-793)

Qy 14 HisProSerArgArgLeuThrGlnGlyArgTPValArgLysSerArgValAlaMetGlu 33
Db 2 CARCTACCGCGACTCACAGGAGATCCAGAGTGTGGAGATCATGGAG 61

34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrrhIleAlaArgAsp 53
Db 62 AAATTCCAGTGTGCACTCTGCTCTGACATCTGGCTACTCTGGCAGAGAT 121

54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
Db 122 ACCCTCTCAACTGCGATTCTGCTCTCTACACTCTGCGCAGAGAT 121

74 ThrIleSerArgGlyLysTgClyAspGlnLeuIlePheGlnThrYgluGluAlaLeu 93
Db 182 ACCCTCTCCAGAGSTGGGTGCAACTCATCGAGCTCAGACATAAGAAGCTTA 241

94 TyrIysSerLysThrSerAsnLysProLeuMetIleLeuLeuAspLysGlu 113
Db 242 TATAATCCAGACAGGACACRAACCCTGATGTTATCATCTGATGTTGCCC 301

114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
Db 302 CACAGTCAGCTTAAAGAAAGTGTGAAATAGAAATCCGAAATGGCAG 361

134 GlnPheValLeuAsnLeuValTYgluThrThrAspLysHisIleSerProAspGly 153
Db 362 CAGTTGCTCTCCATCTGGTTATGAAACAACTGACAACCTTCTCTGATGCC 421

154 GluTyValProArgIleMetPheValAspProSerLeuThrGlnGlyAsp 173
Db 422 CAGTAGT-CCCAGATTATGTTGACCCATCTCTGACAGTTGAAAGCGATCTG 480

174 GlyArgTyrSerAsnArgLeuTyrrAlaTyrrGluProLysAspThrAlaLeuLeuAsp 193
Db 481 GGAAAGATATCNAACCGTCCTATGCTTACAACT-GCAGATAGCCTCTGCTTACACA 539

RESULT 9
US-09-506-421B-78
; Sequence 78 , Application US/09606421B
; Patient No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121-455C9
; CURRENT APPLICATION NUMBER: US/09/606, 421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 78
 LENGTH: 793
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) ... (793)
 OTHER INFORMATION: n = A, T, C or G
 US-09-606-421B-78

Alignment Scores:
 Pred. No.: 8.57e-100 Length: 793
 Score: 856.50 Matches: 177
 Percent Similarity: 94.74% Conservative: 3
 Best Local Similarity: 93.16% Mismatches: 9
 Query Match: 80.57% Indels: 3
 DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-606-421B-78 (1-793)

QY 14 HisProSerArgArchThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33
 Db 2 CATCTAGGCCGACTACACAAGCAGTCAGTGGTGAAGAAATCCAGAGTGCCATGGAG 61

QY 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerIleThrLeuAlaArgAsp 53
 Db 62 AAAATTCACTGTCACTGCACTCTGGCCCTCTCTACACTCTGGCCAAGAGAT 121

QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
 Db 122 ACCACAGTCAACCTGGAGCAAAAGGACACAAGAACCTGCACCAAACCTGCCAG 181

QY 74 ThrlLeuSerArgGlyArgTrpGlyAspGlnLeuIleThrGlnThrGlnThrGln 93
 Db 182 ACCCTCCAGGGTTGGGTGACCAACTCATCGACATAGAGAGCTTA 241

QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleLeuIleHisIleLeu 93
 Db 242 TATAATCCAAAGACAAGAACAAACCTTGATGATTTCATCATCTGGATGTGACTGCCA 301

QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
 Db 302 CACAGTCNAGCTTAAGAAAGTGTGCTGAAATAAGAAATCCAGAAATGGCAAG 361

QY 134 GlnPheValLeuLeuAsnLeuValPheAlaGluIleLeuIleHisIleLeu 153
 Db 362 CAGTTGTCCTCAATCGGTTATGAAACAATCTCCGTGATEGC 421

QY 154 GlnTyrValIleProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
 Db .422 CAGPATGT-CCAGGATATTGTTCTGGCCATCTGACAGTGAAGCCGATATCTG 480

QY 174 GlyArgTyrSerAspArgLeuValPheAlaLeuLeuLeuAsp 193
 Db 481 GGAGCATATGAAACGCTCTCTAGCTACAACT-GCAGATAAGCTCTGTTGCTGACA 539

QY 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203
 Db 540 CAT---GAAAAGCTCAAGTTGCTNAAA 566

RESULT 10
 US-09-221-298-32
 Sequence 32, Application US/09221298
 Patent No. 6284241
 GENERAL INFORMATION:
 APPLICANT: XU, Jiangchun
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF COLON CANCER
 FILE REFERENCE: 210121-471
 CURRENT APPLICATION NUMBER: US/09/221,298
 CURRENT FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 32
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Human
 US-09-221-298-32

Alignment Scores:
 Pred. No.: 4.05e-78 Length: 401
 Score: 683.00 Matches: 132
 Percent Similarity: 98.51% Conservative: 0
 Best Local Similarity: 98.51% Mismatches: 1
 Query Match: 64.25% Indels: 1
 DB: 3 Gaps: 0

US-09-674-266A-181 (1-206) x US-09-221-298-32 (1-401)

QY 57 LysProGlyAlaLysLysAspPheAspArgProLysArgProLysLeuProGlnThrLeuSer 76
 Db 2 ARACCTGGGCCAAAAGACACAAAGGACTCTGACCCAAACTGACCCAGACCCCTCTCC 61

QY 77 ArgGlyTrpGlyAspGlnLeuIleTrpPheGlnGlyAspGluAlaLeuTyrolysser 96
 Db 62 AGACCTGGGTGACCAACTCATGGACTCAGACATATGAAAGAGCTTATAAAATCC 121

QY 97 LysThrSerAsnLysProLeuMetIleLeuIleHisIleLeuAspGluCysProHisSerGln 116
 Db 122 ARGGAAGAACACAAACCCCTGATGATTATTCATCACTGCGGTGTTGCCACACAGTCGA 181

QY 117 AlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaLeuGlnPheVal 136
 Db 182 GCTTAAGAACAAAGTTGCTGAATAATAGAAATAGAAATCCAGAAATTGGAGACAGTTGTC 241

QY 137 LeuIeuAsnLeuValLysGluIleThrAspLysHisIleLeuSerProAspGlyGlntryrVal 156
 Db 242 CTCTCTAACATGTTGTTATGAAACAAACTGACAACACCTTCTCTGATGCCACTATGTC 301

QY 157 ProArgIleMetPheValAspLysPheValAspIleThrGlyArgPhe 176
 Db 302 CCCGGGATTATGTTGTTGACCCATCTCTGACAGTTAGGCCGATATCACTGGAGATA 361

QY 176 rSerAsnArgLeuIleTyrolysrAlaTyrolygluProAlaAspThrAla 189
 Db 362 TTCAACACGCTCTATGCTACGACCTGAGATAACAGT 401

RESULT 11
 US-08-916-576B-35
 Sequence 35, Application US/08916576B
 Patent No. 6171816
 GENERAL INFORMATION:
 APPLICANT: YU, GUO-LIANG
 APPLICANT: DILLON, PATRICK J.
 APPLICANT: EBNER, REINHARD
 APPLICANT: ENDREES, GREGORY A.
 TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: US
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/916,576B
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/024,347
 FILING DATE: 23-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36 688
 REFERENCE/DOCKET NUMBER: 1488.0500001
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (202) 371-2600
 TELEPHONE: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 386 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-16-576B-35

Alignment Scores:
 Pred. No.: 6.51e-73 Length: 386
 Score: 642.00 Matches: 125
 Percent Similarity: 99.22% Conservative: 2
 Best Local Similarity: 97.66% Mismatches: 1
 Query Match: 60.40% Indels: 1
 DB: 3 Gaps: 0

US-09-674-266A-181 (1-206) x US-08-916-576B-35 (1-186)

Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80
 Db 2 CGCAGGACACAAAGGTCTGCACCCAAACTGCCCGAACCTCTCCAGAGTTGGGT 61

Qy 81 AspGlnLeuIleProGlnThrProGlnThrProGlnAlaLeuThrValSerLysThrSerAsn 100
 Db 62 GACA-CATCTGACTAGCATATAAGCTATAATCCAGCAAGCAC 120

Qy 101 LysProLeuMetIleIleHisIleLeuAspGluCysProHisSerGlnAlaLeuLys 120
 Db 121 AAACCCTGATGATTATCATCATCTGGATGACTGGCCACACAGTCAGCTAAAGAA 180

Qy 121 ValPheAlaGluLysLysLysLeuAlaGluLysLeuLeuAspLeu 140
 Db 181 GTTGTGTCGAATAAAGAAATCCAGAACTGCAAGAACTGGCAGTTGCTCTCAATCTG 240

Qy 141 ValTyrrGlnLysSerLysLeuSerProAspGlyGlnTyrrValProArgIleMet 160
 Db 241 GTTATGAAACAATGCAAAACCTTCTCTGATGCCAGATGTCAGTTARG 300

Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrsSerAsnArgLeu 180
 Db 301 TTTGTGACCATCTGACAGTTGACCCGATPATCTGGAGATATTCATCGCTC 360

Qy 181 TyralaTyrgluUroAlaLysPhe 188
 Db 361 TARGCTTACGAAACCTGCGATACA 384

RESULT 12

US-09-643-537-282
 Sequence 282, Application US/09643597
 Patent No. 6426072
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Fan, Liqun
 APPLICANT: Kalos, Michael D.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Hosken, Nancy
 APPLICANT: Ranger, Gary R.
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Sheiky, Yasir A.W.
 APPLICANT: Henderson, Robert A.
 APPLICANT: McNeill, Patricia D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 282
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(404)
; OTHER INFORMATION: n = A,T,C or G
; US-09-643-597-282

Alignment Scores:
 Pred. No.: 1.77e-71 Length: 404
 Score: 631.00 Matches: 125
 Percent Similarity: 92.59% Conservative: 0
 Best Local Similarity: 92.59% Mismatches: 4
 Query Match: 59.36% Indels: 6
 DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-643-597-282 (1-404)

Qy 13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
 Db 16 CGCATCCTANNGCCCACTCACACAGGC-----AGAGTNGCCATG 57

Qy 33 GluLysLeuProValSerAlaPheLeuLeuValAlaLeuSerTyrrThrLeuAlaArg 92
 Db 58 GAGAAATTCCAGTCAGCATTCAGCTTCCTGCTGCGCCCTCTCCTAACCTCTGCCAGA 117

Qy 53 AspThrThrValLysProGlyAlaLysLysAspThrArgProLysLeuPro 72
 Db 118 GATACCAAGCTCAAACCTGNAAGCCAACAAAGGACTCTGACCCAAACTGCCC 177

Qy 73 GluThrLeuSerArgGlyTyrGlyAspGlnLeuIleTrpThrGlnThrGluGluAla 92
 Db 178 CANACCTCTCCAGAGTTGGGTGCAACTCATCGACTCANACATGAAAGACT 237

Qy 93 LeuTyrrLysSerLysSerAsnLysProLeuMetIleIleHisIleLeuAspGluCys 112
 Db 238 CTATATAATCCAGAACAGCAACACCCCTGATGATTATCATCTGATGACTGC 297

Qy 113 ProHisSerGlnAlaLysLysValPheAlaGluLysGluLysGluLeuAla 132
 Db 298 CCACACAGTCAGCTTAAGAAGCTTGTGAAATAAGAAATCCAGAAATCTGCA 357

Qy 133 GluGlnPheValLeuLeuAsnLeuValItyrGluThrThrAspLy 147
 Db 358 GAGCAGTTGCTCTCAATCTGTTATGAAACAACTGCAAA 402

RESULT 13

US-09-48-884A-282
; Sequence 282, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ranger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 282
; LENGTH: 404

TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)...(404)
 OTHER INFORMATION: n = A,T,C or G
 US-09-480-884A-282

Alignment Scores:
 Pred. No.: 1.77e-71 Length: 404
 Score: 631.00 Matches: 125
 Percent Similarity: 92.59% Conservative: 0
 Best Local Similarity: 92.59% Mismatches: 4
 Query Match: 59.36% Indels: 6
 DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-282 (1-404)

Length: 404
 Matches: 125
 Conservative: 0
 Mismatches: 4
 Indels: 6
 Gaps: 1

Qy 13 ProHsProSerArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
 Db 16 CCGCATCTTANNCGCCACTCACAAAGGC-----AGATNGCCATG 57

Qy 33 GluLysIleProValSerAlaPheIleLeuValAlaLeuSerThrLeuAlaArg 52
 Db 58 GAGAAAATTCAAGTCAGATTCTGCTTCCTACACTTGCCAGA 117

Qy 53 AspThrThrValLysProGlyAlaLysAspThrLysAspThrLysAspLysProLeuPro 72
 Db 118 GATACCACAGTCAAACCTGNAGCCAAGAACACAAGGACCAAGGACTCTGACCC 177

Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuIleThrGlnThrThrGluGluAla 92
 Db 178 CANACCTCTCAGAGTTGGGGACCAACTCTGGACTCATCTGGACTCATATGAAAGCT 237

Qy 93 LeuThrLysSerIleSerAspLysProLeuIleLeuSerAspLysAspLys 112
 Db 238 CTATATAATCCAAAGACAAACCAAAACCCCTGTGATTATTCACTGGATGAGTGC 297

Qy 113 ProHisSerGlnAlaLeuLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
 Db 298 CCACACGTCAGCTTAAGAAAGTTGCTGAAATAAGAAATCCGAAATTGGCA 357

Qy 133 GluGlnPheValLeuLeuAsnLeuAsnLysLeuAspGluCys 112
 Db 238 CTATATAATCCAAAGACAAACCAAAACCCCTGTGATTATTCACTGGATGAGTGC 297

Qy 133 LeuThrLysSerIleSerAsnLysProLeuMetIleLeuHisLeuAspGluCys 112
 Db 238 CTATATAATCCAAAGACAAACCAAAACCCCTGTGATTATTCACTGGATGAGTGC 297

Qy 133 GluGlnPheValLeuLeuAsnLeuAsnLysLeuAspGluCys 112
 Db 358 GAGCACTTGCCTCCAAATCTGGTTATGAAACATGCAAA 402

RESULT 14
 US-09-542-615A-282
 Sequence 282, Application US/09542615A
 Patent No. 6518256

GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Fan, Liqun
 APPLICANT: Kalos, Michael D.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Hosken, Nancy A.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aljun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Hosken, Nancy
 APPLICANT: Fanger, Gary R.
 APPLICANT: Li, Samuel X.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 FILE REFERENCE: 210121-455C9

CURRENT APPLICATION NUMBER: US/09/606,421B
 CURRENT FILING DATE: 2000-06-28
 NUMBER OF SEQ ID NOS: 358
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 282
 LENGTH: 404

TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)...(404)
 OTHER INFORMATION: n = A,T,C or G
 US-09-674-266A-181

Alignment Scores:
 Pred. No.: 1.77e-71 Length: 404
 Score: 631.00 Matches: 125
 Percent Similarity: 92.59% Mismatches: 4
 Best Local Similarity: 92.59% Indels: 6
 Query Match: 59.36% Gaps: 1

Percent Similarity:	92.59%	Conservative:	0
Best Local Similarity:	92.59%	Matches:	4
Query Match:	59.36%	Indels:	6
DB:	4	Gaps:	1

US-09-674-266A-181 (1-206) × US-09-606-421B-282 (1-404)

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Qy   13 ProLysProSerArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
Db   16 CGGATCTTANCCGGATTCAACGAGC-----AGAGINGCCRTG 57
Qy   33 GluLysIleProValSerAlaPheLeuIeuLeuValAlaLeuSerTyrThrLeuAlaArg 52
Db   58 GAGAAATTCAGTGTCAACATTCTGCCTCTGCTCTCCTACTCTGCCGA 117
Qy   53 AspThrThrValLysProLysAlaLysAspThrLysAspSerArgProLysLeuPro 72
Db   118 GATACCCAAGTCAAACCTGNAGCCAAAAGGACACAANGACACTCTGCCCAAAACTGCC 177
Qy   73 GluThrLeuSerArgGlyTrpGlyAspGlnLeuIleTrpThrGlnThrYrglUala 92
Db   178 CANACCCCTTCAGGTGGGTGACCACTCATCGACATCANACATATGAGAGCT 237
Qy   93 LysTerTyrLysSerIleSerAsnLysProLeuMetIleIleHisLeuAspGluCys 112
Db   238 CTATATAAATCCAAGACAGCAACAAACCTTGATGATTTCATCATCTGGATGATGTC 297
Qy   113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
Db   298 CCACACAGTCAAAGCTTAAAGAACGTTGCTGAAATAAGAAATTCAGAAATTGCCA 357
Qy   133 GluGlnPheValLeuAsnLeuValTyrGluThrThrAspLys 147
Db   358 GAGCAGTGTGCTCTCATCIGGTTATGAAAACACTGACAAA 402

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Search completed: November 30, 2003, 04:51:26
 Job time : 67 secs

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CM protein - protein search, using sw model

Run on: November 26, 2003, 15:55:59 ; Search time 31 Seconds
(without alignments)

Scoring table: BLOSUM62

Title: US-09-674-266A-181

Perfect score: 1063

Sequence: RLSCAGTLSGSGPHPSRRLT.....DTALLDNMKKALKLKLTEL 206

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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 2: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
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 8: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 9: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 10: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 11: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 12: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 13: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 14: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 15: /cgns_6/picodata/2/pubpaas/pct_New_Pub.pep:
 16: /cgns_6/picodata/2/pubpaas/us10_New_Pub.pep:
 17: /cgns_6/picodata/2/pubpaas/us60_New_Pub.pep:
 18: /cgns_6/picodata/2/pubpaas/us60_New_Pub.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1002	94.3	202	15	US-10-106-698-6395	Sequence 6395, Ap
2	899	84.6	175	10	US-09-792-139-2	Sequence 2, Appl
3	899	84.6	175	12	US-10-237-496-28	Sequence 28, Appl
4	899	84.6	175	12	US-10-242-074-28	Sequence 28, Appl
5	899	84.6	175	12	US-10-242-505-28	Sequence 28, Appl
6	899	84.6	175	12	US-10-242-574-28	Sequence 28, Appl
7	899	84.6	175	12	US-10-243-261-28	Sequence 28, Appl
8	899	84.6	175	12	US-10-243-382-28	Sequence 28, Appl
9	899	84.6	175	12	US-10-243-402-28	Sequence 28, Appl
10	899	84.6	175	12	US-10-243-431-28	Sequence 28, Appl
11	899	84.6	175	12	US-10-245-164-28	Sequence 28, Appl
12	899	84.6	175	12	US-09-903-190-106	Sequence 106, Appl
13	899	84.6	175	12	US-10-244-972-28	Sequence 28, Appl
14	899	84.6	175	12	US-10-197-942-28	Sequence 28, Appl
15	899	84.6	175	12	US-10-238-196-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-106-698-6395
/ Sequence 6395, Application US/101066598
; Publication No. US20030109690A1

GENERAL INFORMATION:

/ APPLICANT: Rubin et al.

/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

/ FILE REFERENCE: PA000P1

/ CURRENT APPLICATION NUMBER: US/10-106-698

/ CURRENT FILING DATE: 2003-03-27

/ PRIORITY APPLICATION NUMBER: PCT/US00/26524

/ PRIOR FILING DATE: 2000-09-28

/ PRIOR APPLICATION NUMBER: US 60/157,137

/ PRIOR FILING DATE: 1999-09-29

/ PRIOR APPLICATION NUMBER: US 60/163,280

/ NUMBER OF SEQ ID NOS: 8564

/ SOFTWARE: PatentIn Ver. 3.0

/ SEQ ID NO: 6395

/ LENGTH: 202

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ FEATURE: MISC_FEATURE

/ NAME/KEY: MISC_FEATURE

/ LOCATION: (1)

/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

/ NAME/KEY: MISC_FEATURE

/ LOCATION: (7)

/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

/ NAME/KEY: MISC_FEATURE

/ LOCATION: (1)

/ OTHER INFORMATION: Best Local Similarity 100.0%; Pred. No. 7,4e-104;

/ Mismatches 0; Indels 0; Gaps 0;

/ Query Match Score 1002; DB 15; Length 202;

/ Matches 194; Conservative 0;

/ Other Information: 94.3%; Score 1002; DB 15; Length 202;

/ Matches 194; Best Local Similarity 100.0%; Pred. No. 7,4e-104;

/ Mismatches 0; Indels 0; Gaps 0;

/ Query Match Score 1002; DB 15; Length 202;

/ Matches 194; Best Local Similarity 100.0%; Pred. No. 7,4e-104;

/ Mismatches 0; Indels 0; Gaps 0;

Qy 13 PHPSSRLTQGRWTKRSVAMEKIPVSASFLLVALSYTLLARDTTKPGAKDTDKNSRKPUP 72
Db 9 PHPSSRLTQGRWTKRSVAMEKIPVSASFLLVALSYTLLARDTTKPGAKDTDKNSRKPUP

FILE REFERENCE: P3630R1C4
; CURRENT APPLICATION NUMBER: US/10/237,496
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065227
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090889
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO: 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-237-496-28

Query Match Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSAFLLIVALSYTLLARDTVPGAKKDTSRKPLPOTLSRGWGDQLIWTQTYEE 91
Db 1 MEKIPVSAFLLIVALSYTLLARDTVPGAKKDTSRKPLPOTLSRGWGDQLIWTQTYEE 60

Qy 92 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 151
Db .1 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 120

Qy 152 DGQYPRIMFVDPSLTVRADITGRYSNRLAYEPADTLIDNMKKALKLKTEL 206
Db .1 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 175

RESULT 4
US-10-237-496-28
; Sequence 28 Application US/10242074
; Publication No. US20030138897A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean Philippe
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLIC
; FILE REFERENCE: P3630R1C19
; CURRENT APPLICATION NUMBER: US/10/242,074
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114

RESULT 3
US-10-237-496-28
; Sequence 28 Application US/10237496
; Publication No. US20030138896A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean Philippe
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLIC
; FILE REFERENCE: P3630R1C19
; CURRENT APPLICATION NUMBER: US/10/242,074
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114

RESULT 2
US-09-792-439-2
; Sequence 2, Application US/09792439
; Patient No. US0020111303A1
; GENERAL INFORMATION:
; APPLICANT: Boyd, Robert Simon
; APPLICANT: Stamps, Alasdair Craig
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
; FILE REFERENCE: 2543-1-005N
; CURRENT APPLICATION NUMBER: US/09/792,439
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004576.5
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: human
US-09-792-439-2

Query Match Score 899; DB 10; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSAFLLIVALSYTLLARDTVPGAKKDTSRKPLPOTLSRGWGDQLIWTQTYEE 91
Db 1 MEKIPVSAFLLIVALSYTLLARDTVPGAKKDTSRKPLPOTLSRGWGDQLIWTQTYEE 60

Qy 92 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 151
Db .1 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 120

Qy 152 DGQYPRIMFVDPSLTVRADITGRYSNRLAYEPADTLIDNMKKALKLKTEL 206
Db .1 ALYSKTSNPKLMITHLDECPSQALKVFAENKEIQQLAEQPVLLNLVYETTDKLSP 175

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 03:27:12 ; Search time 308 Seconds
(without alignments)

Sequence: 2203.591 Million cell updates/sec

Title: US-09-674-266A-181

Perfect score: 1063

Scoring table: BLASTN62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=-cgn2_1/USPTO_spool/US09674266/runat_26112003_152750_15846/app_query.fasta_1.391
-DB=Published_Applications_NA -QFMFT=fastap -SUFFIX=rnpb -MINNMatch=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIXX=blosum62
-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NRH=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09674266 @CGN 1 1 221 @runat_26112003_152750_15846
-NCPUB=3 -ICPU=3 -NO MMAP -LARGEBOUN -NEGS SCORES=0 -WATT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXP=6 -DELEXP=7
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Database : Published_Applications_NA:*

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4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-10-237-496-27

; Sequence 27, Application US/10237496

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Eaton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe

; APPLICANT: Watoube, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Pong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3630R1C4

; CURRENT APPLICATION NUMBER: US/10/237,496

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

SUMMARIES

Result No.	Query Match	Length	DB ID	Description	Sequence 27, Appl
1	1025	96.4	920 12	US-10-237-496-27	

PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-09-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-237-496-27

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203
 Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 96.43% Indels: 1
 DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-237-496-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Db 56 AGACTCGGTGCTGGCACTAGAAACCTTGGCAACTGAGCCACTACA 114

Qy 21 GlngGlyArgTrpValArgYsserArgValAlaMetGluYssleProValSerAlaPhe 40
 Db 115 CAAGCAGTGGTAGGAATCCAGAGTGGCATGGACAAAATTCCAGTGTCAGCAATT 174

Qy 41 LeuLeuLeuValAlaLeuSerTyThrIleAlaArgAspThrThrValYsProGlyAla 60
 Db 175 TTGGCTCCRTGTTGGCCCTCTCCACTCTGGAGAGATACCACAGTCAAACCTGGGCC 234

Qy 61 LysLysAspThrYsAspSerArgProlylLeuProGlnThrLeuSerArgGlyTrpGly 80
 Db 235 AAAAGGAGAACAAAGGACTCTGAGCATATGAGAACCTCTCAAGAGTTGGGT 294

Qy 81 AspGlnLeuIleTrpThrGlnThrTyGluGluAlaLeuTyYsSerIleSerAsn 100
 Db 295 GACCAACTCATGCTGAGATATAATCCAGAACAGAAC 354

Qy 101 LysProLeuMetIleIleAlaIleAspGluCysProHisSerGlnAlaLeuLysYs 120
 Db 355 AAACCTGTTGATGATTATCTACTTGGTGAGTGGCCACAGCTTAAGGAA 414

Qy 121 ValPheAlaGluIwslnlysgluileGlnlysLeuIaGluGlnPheValIeLeuAsnIle 140
 Db 415 GTGTTGCTGAGATATAAGAACATTGAGCACTGGCAGACGTTGTCTCCATACTG 474

Qy 141 ValItyrGluThrThrAspIysHsIleSerProAspGlyGlnIrrValProArgIleMet 160
 Db 475 GTTTGATGAAACAACCTTTCCTGAGCTATGCCAGATGTCAGATTG 534

Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyIgnyTysSerAsnArgIle 180
 Db 535 TTTGTTGACCCATCTCTGAGCTTAGGGGATAATCTGGAGATAATTCAAATCGCTTC 594

Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLybIysAlaLeuYs 200
 Db 115 CAAGGCAAGTGGGTGAGGAAATTCCAGACTTGCATGGGAAATTCCAGACTGTCAGCATTC 174

Db 595 TATGCTTACGAACTGCAGATACAGCTCTGTTGCTGACAACATGAGAAAGCTCTCAAG 654
 Qy 201 LeuLeuIysThrGluIle 206
 Db 655 TrGCTGAGACTGAAATG 672

RESULT 2
 US-10-242-074-27
 Sequence 27, Application US/10242074
 Publication No. US20030138897A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watande, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 CURRENT APPLICATION NUMBER: US/10/242,074
 CURRENT FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: 10,197,942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60,059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60,063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60,065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60,079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60,086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60,087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60,089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60,090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60,090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-242-074-27

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Percent Similarity: 98.54% Conservatives: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 96.43% Indels: 1
 DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-242-074-27 (1-920)

Qy 1 ArgIleSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Db 56 AGACTCGGTGCTGGCACTAGAAACCTTGGCAACTACA 114

Qy 21 GlngGlyArgTrpValArgYsserArgValAlaMetGluYssleProValSerAlaPhe 40
 Db 115 CAAGCAGTGGTAGGAATCCAGAGTGGCATGGACAAAATTCCAGTGTCAGCAATT 174

Qy 41 LeuLeuLeuValAlaLeuSerTyThrIleAlaArgAspThrThrValYsProGlyAla 60
 Db 175 TTGGCTCCRTGTTGGCCCTCTCCACTCTGGAGAGATACCACAGTCAAACCTGGGCC 234

Qy 61 LysLysAspThrYsAspSerArgProlylLeuProGlnThrLeuSerArgGlyTrpGly 80
 Db 235 AAAAGGAGAACAAAGGACTCTGAGCATATGAGAACCTCTCAAGAGTTGGGT 294

Qy 81 AspGlnLeuIleTrpThrGlnThrTyGluGluAlaLeuTyYsSerIleSerAsn 100
 Db 295 GACCAACTCATGCTGAGATATAATCCAGAACAGAAC 354

Qy 101 LysProLeuMetIleIleAlaIleAspGluCysProHisSerGlnAlaLeuLysYs 120
 Db 355 AAACCTGTTGATGATTATCTACTTGGTGAGTGGCCACAGCTTAAGGAA 414

Qy 121 ValPheAlaGluIwslnlysgluileGlnlysLeuIaGluGlnPheValIeLeuAsnIle 140
 Db 415 GTGTTGCTGAGATATAAGAACATTGAGCACTGGCAGACGTTGTCTCCATACTG 474

Qy 141 ValItyrGluThrThrAspIysHsIleSerProAspGlyGlnIrrValProArgIleMet 160
 Db 475 GTTTGATGAAACAACCTTTCCTGAGCTATGCCAGATGTCAGATTG 534

Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyIgnyTysSerAsnArgIle 180
 Db 535 TTTGTTGACCCATCTCTGAGCTTAGGGGATAATCTGGAGATAATTCAAATCGCTTC 594

Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLybIysAlaLeuYs 200
 Db 115 CAAGGCAAGTGGGTGAGGAAATTCCAGACTTGCATGGGAAATTCCAGACTGTCAGCATTC 174

Page 3

PRIOR APPLICATION NUMBER: 60/089801
 / PRIOR FILING DATE: 1998-06-18
 / PRIOR APPLICATION NUMBER: 60/090557
 / PRIOR FILING DATE: 1998-06-24
 / PRIOR APPLICATION NUMBER: 60/090689
 / PRIOR FILING DATE: 1998-06-25
 / Remaining Prior Application data removed - See File Wrapper or PAML.
 / NUMBER OF SEQ ID NOS: 116
 / SEQ ID NO: 27
 / Remaining Prior Application data removed - See File Wrapper or PAML.
 / LENGTH: 920
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 US-10-242-505-27

Qy 41 LeuLeuValAlaLeuSerThrLeuAlaArgSerThrValLysProGlyAla 60
 Db 175 TTGCTCTGGCCCTCTCTACACTGCCAGATACACAGTCACCTGGGCC 234

Qy 61 LysSerAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
 Db 235 AAAAGCACAAAGACTCTGACCAAACTGCCAGACCTCTCAGAGTTGGGT 294

Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluLysLeuThrSerAla 100
 Db 295 GACCACTACCTGGACTAGACATAATGAAAGCTATAATCCAAACACCAAAC 354

Qy 101 LysProLeuMetIleIleHisIleLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
 Db 355 AAACCCCTGATGATTATCATCACTGGATGAGTGCCACAGCTAACAGTTAAGAAA 414

Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuLeuLeu 140
 Db 415 GTGTTGCTGAAATAAGAAATCCGAAATGGCAGAGCAGTTGTCCTCAATCTG 474

Qy 141 ValTygGluThrThrAspLysHisIleSerProAspGlyGlnTyrValProArgIleMet 160
 Db 475 GTTTATGAAACACTGACAAACCTTCTCTGATGCCAGTAGTCAGGATTAG 534

Qy 161 PheValAspProSerLeuIthnvalArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
 Db 535 TTGTTGACCCATCTGACGTTAGGCCATATACTGGAAAGATAATCAATGCTC 594

Qy 181 TYRAlaTYGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysAlaLeuLys 200
 Db 595 TATGCTTAAGACCTGACGTCAGATGCTGTCAGATGAACTGAGCTCTCAAG 654

Qy 201 LeuLeuLysThrGluLeu 206
 Db 655 TTGCTGAAGACTGAAATG 672

RESULT 3
 US-10-242-505-27
 Sequence 27, Application US/10242505
 / PUBLICATION NO: US20030138898A1
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin
 / APPLICANT: Eaton, Dan
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stephan, Jean-Philippe
 / APPLICANT: Watrabe, Colin
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / APPLICANT: Wong, Sherman
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / FILE REFERENCE: P3630R1C25
 / CURRENT APPLICATION NUMBER: US/10/242,505
 / CURRENT FILING DATE: 2002-09-11
 / PRIOR APPLICATION NUMBER: 10/197942
 / PRIOR FILING DATE: 2002-07-18
 / PRIOR APPLICATION NUMBER: 60/059114
 / PRIOR FILING DATE: 1997-09-17
 / PRIOR APPLICATION NUMBER: 60/063046
 / PRIOR FILING DATE: 1997-10-24
 / PRIOR APPLICATION NUMBER: 60/065027
 / PRIOR FILING DATE: 1997-11-10
 / PRIOR APPLICATION NUMBER: 60/079689
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/086478
 / PRIOR APPLICATION NUMBER: 60/087607
 / PRIOR FILING DATE: 1998-06-02

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203
 Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 96.43% Indels: 1
 DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-242-505-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHsProSerArgArgLeuThr 20
 Db 56 AGACTAGCTGCTGCCACACTCAGAGCTT-GAACCGCATCTAGCCGCATCACA 114
 Qy 21 GluGlyArgGlyTrpValArgLysSerArgValAlaMetLysIleProValSerAlaPhe 40
 Db 115 CAAGGGAGGGGGTGGGAAATCAGGTCGCCAGAAATCCAGGAAATCCAGTGTGATTCT 174
 Qy 41 LeuLeuValAlaLeuSerTyrrThrLeuAlaArgAspThrThrValLysProGlyAla 60
 Db 175 TTGTCCTTGTGGCCCTCTCTACACTCTGGCAGATACCAGTCAGTGGAGATAACCTGGGCC 234

Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTPGly 80
 Db 235 AAAAGGACAAAGAACTCTGAACTAAACTGCCAGACCCATCTCCAGAGGTGCGGGT 294

Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeutyrLysSerLysThrSerAsn 100
 Db 295 GACCAACTCACTGGACTCACATGAAAGAGCTATAATCAAGAACGAC 354

Qy 101 LysProLeuMetIleIleHisIleAspGluCysProHisSerGlnAlaLeuLysLys 120
 Db 355 AAACCCCTGATGATTATTCACTCATCACTGGCACACAGCTTAAGAA 414

Qy 141 ValTygGluThrThrAspLysHisIleSerProAspGlyGlnTyrValProArgIleMet 160
 Db 475 GTTAAAGAAACACTGACAACTCTGCTGATGCTCTCTCAATCTGCTC 534

Qy 121 ValPheAlaGluAsnLysGluIleGlnPheValLeuLeuAlaIle 140
 Db 415 GTGTTGCTGAAATAAGAAATTCAGAAATTGGCAGAGCAGTTCTCTCAATCTG 474

Qy 181 TyralaTygGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
 Db 595 TATGCTTAGACCCCTGACAGTTAGCCGATATTCTGAGATTCAATCTGCTC 594

Qy 201 LeuLeuLysThrGluLeu 206
 Db 655 TTGCTGAAGACTGAAATG 672

RESULT 4
 US-10-242-574-27
 Sequence 27, Application US/10242574
 / PUBLICATION NO: US20030138898A1
 / GENERAL INFORMATION:

ORGANISM: Homo Sapien
US-10-243-261-27

Alignment Scores:
Pred. No.: 1.33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 95.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) × US-10-243-261-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrIleSerGlySerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCACTGTCCTGCCAGACACTCAGAAGCTT-GGACCGCATCTAACCGGGACTACA 114
Qy 21 GlnglyArgtrpValArgLysserSerArgValAlaMetGluValLeProlvalSerAlaPhe 40
Db 115 CAGGGCAGTGGTGGTGAGGAATCCAGGTGGCATGGAAAATTCCAGTGTCAAGATTC 174
Qy 41 LeuLeuIeuaValAlaLeuSerIrrthreuaAlaArgAspThrThrVallyProGlyAla 60
Db 175 TGTCTCTGTGCCCrTCACACTGGCCAGATAACACAGTCAAACCTGGAGCC 234
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAGGCACAAAGGACTCTGACCCAAACTGCCAGAACCTCTCAGGGTTGGGT 294
Qy 81 AspGlnLeuIlePhePheGlnThrArgIleGluAlaLeuTyrySerIrrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAAAGCTATAATCAGAACACAC 354
Qy 101 LysProLeuMetIleIleHISIleLeuAspGluCysProHisSerGlnAlaLeuLys 120
Db 355 AAACCTTGATGATTATCATCACITGATGATGTCACAGTCAGCTTAAGAAA 414
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAla 140
Db 415 GTGTTGGAAAAATAAGAAATCCAGAAATTGGCAGAACCTTGCAAGATPATCCTC 474
Qy 141 ValTyrgluthrThrAspLysIleSerProAspGlyGlnTrpValProArgileMet 160
Db 475 GTTATGAAACACTGACAAACACTGACAAACCTTCTCTGAAGGCCAGTAGTCAG 534
Qy 161 PheValAspProSerIleThrValIleGlnLysLeuAlaGluGlnPheValLeuLeu 180
Db 535 TTGTTGACCCATCTCAGACTAGGCCGATATCATGGAGAATPATCCTC 594
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsnMetLysLysAlaLeuLys 200
Db 595 TAGCTTACGAACTGCAAGATACAGCTGTGCTTGTGCAACATGAGAAAGCTCTCAAG 654
Qy 201 LeuLeuIrrSerIleLeu 206
Db 655 TTGCTGAAGACTGAATG 672

RESULT 6
US-10-243-282-27
Sequence 27, Application US/10243282
Publication No. US20030138901A1
GENERAL INFORMATION
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Pilvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P3630PLC50
CURRENT APPLICATION NUMBER: US/10/243,282
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/099801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 27
LENGTH: 920
TYPE: DNA
ORGANISM: Homo Sapien
US-10-243-282-27

Alignment Scores:
Pred. No.: 1.33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservativeness: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0
US-09-674-266A-181 (1-206) × US-10-243-282-27 (1-920)
Qy 1 ArgLeuSerCysAlaIleIleHISIleLeuAspGluCysProHisSerGlnAlaLeuThr 20
Db 56 AGACTCACTGTCCTGCCAGACACTCAGAAGCTT-GGACCGCATCTAACCGGGACTACA 114
Qy 21 GlnglyArgtrpValArgLysserSerArgValAlaMetGluValLeProlvalSerAlaPhe 40
Db 175 TGTCTCTGTGCCCrTCACACTGGCCAGATAACCTGGAGCC 234
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAGGCACAAAGGACTCTGACCCAAACTGCCAGAACCTCTCAGGGTTGGGT 294
Qy 81 AspGlnLeuIlePhePheGlnThrArgIleGluAlaLeuIrrLysSerIrrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAAAGCTATAATCAGAACACAC 354
Qy 101 LeuLeuValAlaIleSerIrrSerIrrLeuSerGlySerGlyProSerArgArgLeuThr 20
Db 355 TTGCTTGGCCCTCTCTACTCTGAGATTCAGCTGAGAAATTCAACCTGGAGCC 114
Qy 121 ValGlnIgYArgTrpValArgLysserSerArgValAlaMetGluValLeProlvalSerAlaPhe 40
Db 415 CAAGGZGAGTGGTGAGGAATTCGCAAGTCCCATGAGAAATTCAACCTGGAGCC 234
Qy 141 ValTyrgluthrThrAspLysIleSerProAspGlyGlnTrpValProArgileMet 160
Db 475 GTTATGAAACACTGACAAACCTTCTCTGAAGGCCAGTAGTCAG 534
Qy 161 PheValAspProSerIleThrValIleGlnLysLeuAlaGluGlnPheValLeuLeu 180
Db 535 TTGTTGACCCATCTCAGACTAGGCCGATATCATGGAGAATPATCCTC 594
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsnMetLysLysAlaLeuLys 200
Db 595 TAGCTTACGAACTGCAAGATACAGCTGTGCTTGTGCAACATGAGAAAGCTCTCAAG 654
Qy 201 LeuLeuIrrSerIleLeu 206
Db 655 TTGCTGAAGACTGAATG 672

Qy 101 LysProLeuMetIleIleHISIleLeuAspGluCysProHisSerGlnAlaLeuIrrLys 120
Db 355 AAAAGACACAAAGGACTCTGACCCAAACTCTGAGCTCTCACAGGGCTGGGT 294
Qy 81 AspGlnLeuIlePhePheGlnThrArgIleGluAlaLeuIrrLysSerIrrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAGAAAGCTCAACCTGGAGCC 234
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAGACACAAAGGACTCTGACCCAAACTCTGAGCTCTCACAGGGCTGGGT 294
Qy 81 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluIrrLeuLeuAsnLeu 140
Db 415 GTGTTGCTGAAATAAGAAATTCAGAAATTGGAGAGTTGCTCTCATCTG 474
Qy 141 ValTyrgluthrThrAspLysIleSerProAspGlyGlnTrpValProArgileMet 160

Db 475 GTTATGAAACAACCTGACAACTGATGCCAGATGTCCCAGGATPATG 534
 Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThreGlyArgTyrSerAsnArgLeu 180
 Db 535 TTGTTGACCATCTTGACGTAGGCCATATCAGTGA 594
 Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuAspMetLysAlaLeu 200
 Db 595 TAGCTTACACCTGAGATAACAGCTGTGCTGACATGAAGCTCAAG 654
 Qy 201 LeuLeuLysThrGluLeu 206
 Db 655 TTGCTGAAAGACTGATTG 672

RESULT 7
 US-10-243-402-27
 Sequence 27, Application US/10243402
 Publication No. US20030138902A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watanabe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILE REFERENCE: P3630R1C39

CURRENT APPLICATION NUMBER: US/10/243,402
 CURRENT FILING DATE: 2003-09-12
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-243-402-27

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203
 Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 96.43% Indels: 1
 DB: 12 Gaps: 0

US-09-674-266a-181 (1-206) x US-10-243-402-27 (1-920)
 Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerClyProHisProSerSerClyProHisProSerArgArgLeuThr 20
 Db 56 AGACTACGTCGTCGGACACTCAGAGCTT GGACCGCATCTAGCCGCCTACTCACCA 114
 Qy 21 GlngLyA9gTpvA9gLySsArgValAlaMetGluYB1leProlvalSerAlaPhe 40
 Db 115 CAGGCCAGTGTTGAGGAAATCAGACTGAGTGCATGGAAATTCCAGTGTGCAAGCANTC 174
 Qy 41 LeuLeuLeuValAlaLeuSerYrrThrLeuAlaArgAspThrThrValYsProGlyAla 60
 Db 175 TGGCTCTGTGCCCTCACACTGGCAGATAACAGTGTAACTGGAGCC 234
 Qy 61 LysLyAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrgLy 80
 Db 235 AAAAGGACAAAGGACTCTGACCCAACACTGACCTCTCCAGAGCTTCAGAGTTGGGT 294
 Qy 81 ABG11LeuIlePhePheGlnThrYsGluGluAlaEutYsSerLysThrSerAsn 100
 Db 295 GACCAACATCTGGACTCAGACATATAAAAGCTATAAAATCCAAAGAACGACAC 354
 Qy 101 LysProLeuMetIleIeHsIleAspGluCysProHisSerGlnAlaLeuLybLyb 120
 Db 355 AACCTCTGATGATTATCATCTGATGATGATGCTGCCCCACACGTCAAGCTTAAGGAA 414
 Qy 121 ValPheAlaGluAsnLysGluIleGlyDileAlaGluGlnPheValLeuLeuAlaLeu 140
 Db 415 GTGTTGCTGAAATAAGAAATCCAGAAATTGGCAGCAGTTGCTCTCCATCATCTG 474
 Qy 141 ValYsGluThrPheAspLysIleSerProAspGlyGlnTrYrValProArgIleMet 160
 Db 475 GTTTGTGAAACAACTGACAAACCTCTCTCTCTGATGCTGCCACTATGTTCCCCGGATATG 534
 Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThreGlyArgTyrSerAsnArgLeu 180
 Db 535 TTGTTGACCCATCTCTGACGTTAGCCGATATCTGAAAGATTCATCTGATCTGTC 594
 Qy 181 TYTAAIaTyrGluProAlaAspThrAlaLeuLeuAspAsnMetIlysLysAlaLeu 200
 Db 595 TATGTTACGAACTGGAGATACTGCTGCTGCTGAAAGCTCTCAG 654
 Qy 201 LeuLeuLysThrGluLeu 206
 Db 655 TTGCTGAAAGACTGAAATG 672

.RESULT 8
 US-10-243-411-27
 Sequence 27, Application US/10243431
 Publication No. US20030138903A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watanabe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 APPLICANT: Title of Invention: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630R1C37
 CURRENT APPLICATION NUMBER: US/10/243,431
 CURRENT FILING DATE: 2002-09-12
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-243-402-27

PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079659
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-55
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 27
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-243-431-27

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203
 Percent Similarity: 90.54% Conservative: 0
 Best Local Similarity: 96.54%
 Query Match: 96.43%
 DB: 12
 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-431-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrIleSerGlySerArgProHisProSerArgArgLeuThr 20
 Db 56 AGCTCACTGGTGGACACTAGAGCTTGAAATCCAGTCAGCGATCACA 114

Qy 21 GlnGlyArgTrpValArgLysserArgValAlaMetGluLysileProValSerAlaPhe 40
 Db 115 CAGGCAGGTGGCTGAGAAATTCCAGTCAGGTTGCCATGGAAATACTCCAGTCAGCATTC 174

Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuIleArgLysThrThrValYProGlyAla 60
 Db 175 TRGCTCTGTGGCCCTCTCCATACCTGGCCAGAGATACCACAGTCAAACCTGGAGCC 234

Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyLysGly 80
 Db 235 AAAAGGACACAAAGGACTCTGACCAAACTGCCAGACCTCTCAGGGTGGGT 294

Qy 81 AspGlnIleIleIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
 Db 295 GACCAACATCATCTGGACTCAGACATATGAAAGAGCTTATAATCCAAGACAAC 354

Qy 101 LysProIsoleucineLeuAspGluCysBProHisSerGlnAlaLeuLysLys 120
 Db 355 AAACCCCTGATGATTATCATACTGGATGAGTGGCCACACAGTCAGCTTAAGAAA 414

Qy 121 ValPheAlaGluAsnLysLeuIleGluGlnPheValLeuLeuLeuLeu 140
 Db 415 GTGTTGGATAATAAGAAATCCAGAAATTGGCAGAGCAGTTCCTCAATCTG 474

Qy 141 ValTyrgluIleThrAspLysHisIleSerProAspGlyGlnTyrValProArgIleMet 160
 Db 475 GTTATGAAACACTGAAACACCTTCTCTGATGCCAGTATGCCAGGATTAG 534

Qy 161 PheValAspProSerIleThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
 Db 535 TTGTTGATGCCATCTGACAGTTAGGCCGATATCACGGAAAGATATCGTC 594

Qy 181 TyrAlaTyrGluProAlaAspHrrAlaLeuLeuLeuAspAlaMetLysSerAlaLys 200
 Db 595 TATGCTTAGAACACTGAGATACTGTTGCTGAGTCTGTTGCTGAGCATTC 654

Qy 201 LeuLeuLysThrGluLeu 206
 Db 655 TTGCTGAAGACTGAAATTCCAGTGTGCAATGGAGAAATTCCAGTGTGCACTTC 672

RESULT 9
 US-10-245-164-27
 Sequence 27, Application US/10245164
 Publication No. US20030138904A1
 GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin
 / APPLICANT: Baton, Dan
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stephan, Jean-Philippe
 / APPLICANT: Watande, Colin
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / APPLICANT: Fong, Sherman
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 / FILE REFERENCE: P363081C76
 / CURRENT APPLICATION NUMBER: US/10-245,164
 / CURRENT FILING DATE: 2002-09-16
 / PRIOR APPLICATION NUMBER: 10/197942
 / PRIOR FILING DATE: 2002-07-18
 / PRIOR APPLICATION NUMBER: 60/059114
 / PRIOR FILING DATE: 1997-09-17
 / PRIOR APPLICATION NUMBER: 60/063046
 / PRIOR FILING DATE: 1997-10-24
 / PRIOR APPLICATION NUMBER: 60/065027
 / PRIOR FILING DATE: 1997-11-10
 / PRIOR APPLICATION NUMBER: 60/079689
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/086478
 / PRIOR FILING DATE: 1998-05-22
 / PRIOR APPLICATION NUMBER: 60/087607
 / PRIOR APPLICATION NUMBER: 60/089801
 / PRIOR FILING DATE: 1998-06-18
 / PRIOR APPLICATION NUMBER: 60/090557
 / PRIOR FILING DATE: 1998-06-24
 / PRIOR APPLICATION NUMBER: 60/090689
 / PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PAM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO: 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-245-164-27

Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203
 Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 96.43% Indels: 1
 DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-245-164-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgGluLeuThr 20
 Db 56 AGACTCAGCTGGCAGACTCGCTGAGCAGTCTGGCAGACTCTGAAAGCTT-GAACCGCATCTGCTGGCACACTCGAAGCTT-GAACCGCATCTGCTGGCAGACTCTGCA 114

Qy 21 GlnGlyArgTrpValArgLysserArgValAlaMetGluLysileProValSerAlaPhe 40
 Db 115 CAAGGCAAGGTGGTGGAGGAAATCCAGTCAGGTTGCCATGGAAATACTCCAGTCAGCATTC 174

Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuIleArgLysThrThrValYProGlyAla 60
 Db 175 TATGCTTAGAACACTGAGATACTGTTGCTGAGTCTGTTGCTGAGCATTC 654

Qy 41 LeuIleLeuValAlaLeuSerTyrThrLeuIleArgLysThrThrValYProGlyAla 60

Db 175 TTGCTCCRTGGCCCTCCTACACTCGGCCAGAGATAACCACAGTAACTGGACCC 234 ; PRIOR APPLICATION NUMBER: 60/090557
 Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80 ; PRIOR FILING DATE: 1998-06-24
 Db 235 AAAAGGACACAAGGACTCTGACCCAAACTGCCAGACCCCTTCAGAGGTGGGT 294 ; PRIOR APPLICATION NUMBER: 60/090689
 Db 81 AspGlnLeuIleTrpThrGlnThrSerGlnAlaLeuTyrosSerIleSerAsn 100 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 Qy 295 GACCACTGAGCATGAGATAGACATGAGATAATGAGAACGACAAAC 354 ; SEQ ID NO: 27
 Db 101 LysProLeuMetIleIleHisHisLysLeuAppGluLysProLysLeuLysLys 120 ; TYPE: DNA
 Db 355 AAACCTTGATGATTATCATCACTTGGTAGTGAATGCCACACTCAACCTTAAGAAA 414 ; ORGANISM: Homo Sapien
 Qy 121 ValPheAlaGluLysLysBgluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140 ; SEQ ID NOS: 116
 Db 415 GTGTTGCTGAAATAAAGAAATCCAGAAATTGGCAGACGAGTCCTCCATCTG 474 ; LENGTH: 920
 Qy 141 ValTyrgLutIleThrAspIleHisIleSerProLysGlyGlnTyrvAlaProArgIleMet 160 ; US-10-244-972-27
 Db 475 GTTATGAAACAACGACAAACCTTICCTCATGGCAGATGTCAGATTG 534 ; Alignment Scores:
 Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrsSerAsnArgLeu 180 ; Pred. No.: 1.33e-130
 Db 535 TTGTTGACCCATCTGCACATGAGCCGATATCACTGGAAAGATAATCGTC 594 ; Score: 1025.00
 Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuAsnAsnNetLysLysAlaLeuLys 200 ; Percent Similarity: 98.54%
 Db 595 TATGTTTACGAAACCTGCAGATAACAGCTCTGTGCTTGACAAATGAAAGCTCTCAAG 654 ; Best Local Similarity: 98.54%
 Qy 201 LeuLeuLysIleThrGlnIleSerProLysGlyGlnTyrvAlaLeu 206 ; Query Match: 96.43%
 Db 655 TTGCTGAAACTGAGCTGATTG 672 ; DB: 12
 Db 175 TTGTTCCCTGTGSCCTCCPACACTCTGGCCAGAGATAACCTGGACCC 234 ; Length: 920
 Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80 ; Matches: 203
 Db 235 AAAAGGACACAAGGACTCTGCCAAACTGCCAGACCCAAACTGGCCAGCTCTCCAGAGGTGGGT 294 ; Conservative: 0
 Qy 81 AspGlnLeuIleTrpThrGlnThrValGluAlaLeuTyrosSerIleThrSerAsn 100 ; Mismatches: 3
 Db 295 GACCAACTCATCTGGACTCAGACATATAATCCAGAACGACAC 354 ; Indels: 1
 Qy 101 LysProLeuMetIleIleHisIleLeuAspGluCysProHisSerGlnAlaLeuLys 120 ; Gaps: 0
 Db 355 AAACCTTGAAATAAAGAAATCCAGAAATTGGCAGACCTGCTCCATCTG 474 ;
 Qy 141 ValTyrgLutIleThrAspIleHisIleSerProAspGlyGlnTyrvAlaProArgIleMet 160 ;
 Db 475 GTTATGAAACAACGACAACTGCAAAACCTTCTCTGATGCCCAGATTG 534 ;
 Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrsSerAsnArgLeu 180 ;
 Db 535 TTCTGTGAAATAAAGAAATCCAGAAATTGGCAGACCTGCTCCATCTG 474 ;
 Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuAsnNetLysLysAlaLeu 200 ;
 Db 595 TATGTTTACGAAACTGAGATAACAGCTCTGTGCTTGACAAATGAAAGCTCTCAAG 654 ;
 Qy 201 LeuLeuLysIleThrGlnIleSerProLysGlyGlnTyrvAlaLeu 206 ;
 Db 655 TTGCTGAAACTGAGCTGATTG 672 ;
 RESULT 11 ;
 US-10-244-972-27 ; Sequence 27, Application US/10244972
 ; Sequence 27, Application US/10244972
 ; GENERAL INFORMATION:
 ; Publication No. US20030170809A1
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; APPLICANT: Fong, Sherman
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630R1C75
 ; CURRENT APPLICATION NUMBER: US10/244,972
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; Sequence 27, Application US/10197942
 ; Publication No. US20030175882A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Eaton, Dan

PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145598
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: 60/178857
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/179857
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/198587
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PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/213371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-07-13
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PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: 60/213371
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PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
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PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/26150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C1 (US)
CURRENT APPLICATION NUMBER: US/10/197,942
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
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PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/282129
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/282199
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/290589
 PRIOR FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: 09/180997
 PRIOR FILING DATE: 1998-11-19
 PRIOR APPLICATION NUMBER: 09/267213
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 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: 09/423741
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: 09/709238
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 09/02706
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 09/372035
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: 09/318585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 09/324419
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: 09/327796
 PRIOR FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/329404
 PRIOR FILING DATE: 2001-08-13
 PRIOR APPLICATION NUMBER: 09/331836
 PRIOR FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: 09/341992
 PRIOR FILING DATE: 2001-08-28
 PRIOR APPLICATION NUMBER: 09/46374
 PRIOR FILING DATE: 2001-09-04
 PRIOR APPLICATION NUMBER: 10/001054
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 10/081056
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: 10/19480
 PRIOR APPLICATION NUMBER: PCT/US98/18824
 PRIOR FILING DATE: 1998-09-10

Alignment Scores:
 Pred. No.: 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Score: 1.33e-130 Length: 920
 Percent Similarity: 1025.00 Matches: 203
 Best Local Similarity: 98.54% Conservative: 0
 Query Match: 96.43% Mismatches: 3
 DB: 12 Indels: 1
 Gaps: 0

US-09-674-266A-181 (1-206) × US-10-197-942-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
 Db 56 AGACTCAGCTGTGCGCACTGAAACCTGGCCATCTAGGCCGACTCA 114

Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaNetGluLysIleProValSerAlaPhe 40
 Db 115 CAAGGCCAGTGGCTCAGGAATCCAGTGGCCATTCCAGTGGCCATT 174

Qy 41 LeuLeuLeuValAlaLeuSerItyThrLeuAlaArgAspThrThrVallysProGlyAla 60
 Db 175 TTGCCTCTTGCCCTCCTGAGATCACGTAACCTGGAGCC 234

Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80

Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-238-196-27

Alignment Scores:
Pred. No.: 1.33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 95.54% Conservative: 0
Best Local Similarity: 98.54%
Query Match: 96.43%
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-238-196-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrIleuSerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCACTGCTGCTGCACTAGAGCTT-GGACGCCATCTACCGGGACTACA 114

Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
Db 115 CAAGGCAGTGCTGCTGCAAGAAATTCCAGATGCGATTCAGAAATACTCGATTC 174

Qy 41 LeuLeuLeuValAlaLeuSerItyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
Db 175 TGGCTCTGTGGCCCTCTCTACTCTGGCAGAGTACACAGTCAAACCTGAGCC 234

Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGLYTrpGLY 80
Db 235 AAAAGGCAACAAAGGACTCTGACCAAAACTGCCAGAACCTCTCAGAGTTGGGT 294

Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuThrLysSerItyrVal 100
Db 295 GACCAACTCATCTCGACTCAGACATATGAGAGCTCTATAATCAAGCAAAAC 354

Qy 101 LysProLeuMetIleIleHistidineLeuAspGluCysProHisSerGlnAlaLeuLys 120
Db 355 AAACCCTTGATGATTATCATACTGGATGAGTGGCCACACAGTCAGCTTAAGAAA 414

Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
Db 415 GTGTTGCTGAATAAGAAATCCAGAAATGGCACAGTGTGACTTCATCTG 474

Qy 141 ValTyrgluthThrAspLysIleSerProAspGlyGlnTyrValProArgIleMet 160
Db 475 GTTATGAAACACTGACAAACACCTTCTCTGATGCCACTATGTCAGGATTAG 534

Qy 161 PheValAspProSerIleThrValArgAlaAspIleThrGlyArgTyrsSerAsnArgLeu 180
Db 535 TTGTTGCAACCATTCTGACATTAGGGCGATATGCTGAGATTCATCTGTC 594

Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysAlaLeuLys 200
Db 595 TAGCTTAGAACCTGAGATAAGCTGTGCTGACAACATGAGAAAGCTCTGAG 654

RESULT 13
US-10-245-013-27
; Sequence 27, Application US/10245013
; Publication No. US/030186373A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: 355 AAACCTTGATGATTACATCACTGGTCAAGTGGCTAACAGTAAARGAAA 414

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Qy 121 Val Phe Ala Glu Asn Lys Glu Leu Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Ile 140
 Db 415 GTGTTTGCTGAAATAAGAAATTCAGAAATTGGCAGAGCAATTGCTCCUAACTTG 474
 Qy 141 Val Tyr Glu Ile Thr Asp Lys His Leu Ser Pro Asp Gly Glu Ile Val Pro Arg Ile Met 160
 Db 475 GTTATGAACACTGACAAACCTTCTCCGTATGCCAGATGTCAGATTG 534
 Qy 161 Phe Val Asp Pro Ser Leu Thr Val Asp Ile Thr Gly Arg Tyr Ser Asn Arg Ile 180
 Db 535 TTCTTGACCCATCTGCACGTTAGCCGATATCACTGGAGATATTCAAATCGTCTC 594
 Qy 181 Tyra Lys Glu Pro Alanine Pro Alanine Pro Alanine Leu Leu Asn Met Lys Lys Ile Leu Ile 200
 Db 595 TATCTTAGAACCTGCAAGATAGCTCTGTTGAAACATGAAAGAARGSTCTGAG 654
 Qy 201 Leu Leu Lys Ile Ser Tyr Thr Leu Val Arg Asp Thr Val Lys Pro Glu Ala 60
 Db 655 TTGCTGAACTGACTGATTG 672
 Db RESULT 14
 US-10-245-103-27
 Sequence 27, Application US/10245103
 Publication No. US20030068778A1.
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Flivroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Waranbe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3650R1C112
 CURRENT APPLICATION NUMBER: US/10/245,103
 CURRENT FILING DATE: 2002-09-17
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NO'S: 116
 SEQ ID NO 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-245-103-27
 Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203

Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 3
 Query Match: 14% Deletions: 1
 Gaps: 0
 US-09-674-266A-181 (1-206) × US-10-245-103-27 (1-920)
 Qy 1 Arg Leu Ser Cys Ala Gly Thr Ile Ser Lys Ser Gly Pro His Pro Ser Arg Arg Leu Thr 20
 Db 56 AGCTCACTGCTCTGGCACTGGCACTGAGGCTT GGCGCATCTAGCCGACTACA 114
 Qy 21 Glu Gly Arg Trp Val Arg Lys Ser Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe 40
 Db 115 CAAGCAGTGGTGGTGGAAATCGAGCTGGCATGGAAATTCCAGTGTCACTTC 174
 Qy 41 Leu Leu Leu Val Ala Leu Ser Tyr Thr Leu Val Arg Asp Thr Val Lys Pro Glu Ala 60
 Db 175 TTGGTCCCTTGTCGCCCTCTCCPACACTCTGGCCAGAGTACACAGTCAAACCTGGAGAC 234
 Qy 61 Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Leu Pro Glu Ile Thr Leu Ser Arg Gly Tyr Pro Gly 80
 Db 235 AAAAGGCAAAAGGACTCTGCCAACACTCCAGAGCTTCCAGAGTTGGGT 294
 Qy 81 Asp Glu Leu Ile Thr Glu Glu Val Leu Tyr Lys Ser Lys Thr Ser Asn 100
 Db 295 GACCAACTCATCTGACTGAGCTAGCATGATATAATCCAGAACAGAAC 354
 Qy 101 Lys Pro Leu Met Ile Ile His Ile Leu Asp Glu Cys Pro His Ser Gln Alanine Lys Ile 120
 Db 355 AAACCCTTGATGATTATCATCATCTGATGACTGCCCACACAGTCAAGCTTAAGAAA 414
 Qy 121 Val Phe Ala Glu Asn Lys Glu Ile Glu Ile Glu Lys Leu Ala Glu Glu Ile Phe Val Leu Leu Ileu 140
 Db 415 GTGTTGCTGAAATAATGAAATCAGAAATTCGAGTTGCAAGTGTCTCTCAATCTG 474
 Qy 141 Val Tyr Glu Ile Thr Asp Dly His Leu Ser Pro Asp Gly Glu Ile Val Pro Arg Ile Met 160
 Db 475 GTTTATGAAACACTGACAAACCTTCTCCAGATGTCAGATGTCAGATTG 524
 RESULT 15
 US-10-245-107-27
 Sequence 27, Application US/10245107
 Publication No. US20030068779A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Flivroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Stephan, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watane, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3650R1C112
 CURRENT APPLICATION NUMBER: US/10/245,103
 CURRENT FILING DATE: 2002-09-17
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 NUMBER OF SEQ ID NO'S: 116
 SEQ ID NO 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-245-103-27
 Alignment Scores:
 Pred. No.: 1.33e-130 Length: 920
 Score: 1025.00 Matches: 203

TYPE: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ORGANISM: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630R1C71
 CURRENT APPLICATION NUMBER: US/10/245,107
 CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 27
 LENGTH: 920
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-245-107-27

Alignment Scores:

	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Deletes:	Gaps:
Qy	1	ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr	920	920			920	203	0			
Db	56	AGACTCAGCTTGCGCACACTCGAGCTAGAACGCT-GGACCGCATCCTAGCCGCCGACTCACCA										114
Qy	21	GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe	40	40								
Db	115	CAAGGGAGGTTGGGTGAGGAATTCAGAGTGCATGCCATGGAAAATTCCAGGTGTCAGCATC										174
Qy	41	IleLeuLeuValAlaIeuSerTyrrLeuAlaArgAspThrThrValLysProGlyAla	60	60								
Db	175	TTCGCTCTGGCCCTCTCCACTCTGAGATACACTCGCCAGAGATACACACTCAACCTGGGCC										234
Qy	61	LysLysAspThrLysAspSerArgProLysIleProGlnThrLeuSerArgGlyTyrGly	80	80								
Db	235	AAAANGACAACAAAGGACTCGACCACAAACTGCCAGACGATTAATCCAGAACGCAAC										294
Qy	81	AspGinLeuIleTrpThrGlnThrTyrGluGluAlaLysTyrLysSerIleSerAsn	100	100								
Db	295	GACCAACTCACTGGACTAGATTCATCAGTCAGATGAGCTATAATCCAGAACGCAAC										354
Qy	101	LysProLeuMetIleIleHighHiIleLeuAspGluCysProHisSerGlnAlaLeuLys	120	120								
Db	355	AAACCCCTTGATGATTACATCAGTCAGATGAGCTATAATCCAGAACGCAAC										414
Qy	121	ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuAsnLeu	140	140								
Db	415	GTGTTGCTGAAATAAGAATCCGAATTCGAAATTGGCAAGGAGTGTCTCCTCAATCTG										474
Qy	141	ValTyrGluIleThrAspLysHisIleSerProAspGlyGlnTyrValProArgIleMet	160	160								
Db	475	GTTATGAAACAGCTGACAACACCTTCTCTGATGCCAGTATGCCAGGATTARG										534
Qy	161	PheValAspProSerLeuThrValAlaGlnAspIleThrGlyArgTyrSerAsnArgLeu	180	180								
Db	595	TTTGTGTTGACCCCATCTGATGTTGAGCCGATATACCTGAGATATTGATGATGATG										594

Search completed: November 30, 2003, 05:00:53
 Job time : 311 secs

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OM protein - protein search, using sw mode!

Run on: November 26, 2003, 15:52:53 ; Search time 21 Seconds
 (without alignments)
 943.369 Million cell updates/sec

Title: US-09-674-266A-181
 Perfect score: 1063
 Sequence: 1 RLSCAGTLSGSGPHPSRRLT.....DTALLDNMKKALKLKLTEL 206

Scoring table: BL05162
 GapOp 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	899	84.6	175	2 JB0350	Anterior gradient-hypothetical protein
2	199	18.7	186	2 T31643	probable protein d
3	119	11.2	150	2 D61100	hypothetical prote
4	87.5	8.2	458	2 S50919	probable disulfide
5	87	8.2	348	2 G72016	disulfide bond iso
6	87	8.2	348	2 C86607	myosin-V - chicken
7	85.5	8.0	1830	1 S19188	probable peptidogl
8	84.5	7.9	1151	2 AG1717	hypothetical prote
9	84	7.9	771	2 S51421	probable transcript
10	83.5	7.9	217	2 T37859	unknown protein F1
11	83.5	7.9	918	2 C96829	cell cycle protein
12	83	7.8	479	2 T40683	lipopeptide protein
13	83	7.8	507	2 S56143	phosphatidylinosit
14	82	7.8	788	2 C70441	insitol polyphosph
15	81.5	7.7	893	2 G59431	probable protein d
16	81.5	7.7	970	2 S22069	F14023.14 .Importe
17	81.5	7.7	1158	2 T50454	probable rho GDP-
18	81.5	7.7	1397	2 T10466	DNA topoisomerase
19	81	7.6	610	2 T22909	hypothetical prote
20	81	7.6	635	2 T23874	probable protein
21	80	7.5	154	2 P82633	hypothetical protein
22	80	7.5	259	2 A96740	F14023.14 .Importe
23	80	7.5	843	2 S531947	hypothetical prote
24	79.5	7.5	277	2 T37629	GTP-binding protei
25	79.5	7.5	301	2 G71929	ABC transporter (A
26	79.5	7.5	642	2 F83718	hypothetical prote
27	79.5	7.5	921	2 F84593	probable rna polym
28	79	7.4	477	2 T37791	carboxypeptidase C
29	79	7.4	510	1 S43516	

ALIGNMENTS

RESULT 1						
JB350	Anterior gradient-2 - human	C;Species: Homo sapiens (man)	C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000			
	R;Thompson, D.A.; Weigel, R.J.	Biochem. Biophys. Res. Commun. 251, 111-116, 1998	A;Title: hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is cross-reactive with the mouse anti-XAG-2 antibody			
		A;Reference number: JE0350; PMID:9790916	A;Cross-references: GB:AP007791; NID:93779196; PIDN: AAC77358.1; PMID:93779197			
		A;Accession: JE0350	C;Comment: This protein is coexpressed with estrogen receptor (ER) in breast cancer cell line MCF-7.			
		A;Molecule type: mRNA	C;Genetics:			
		A;Residues: 1-175 <TH0>	A;Gene: hAG-2			
		C;Superfamily: human anterior gradient-2				
Query	MEKIPVSAILLVALASYTLLARDTIVPQAKKDTKDSRKPQTKPGLQTLSRGWGDOLIWTOTYEE 91	Match	84.6%; Score 899; DB 2;	Length 175;		
Matches	1 MEKIPVSAILLVALASYTLLARDTIVPQAKKDTKDSRKPQTKPGLQTLSRGWGDOLIWTOTYEE 60	Best Local Similarity	100.0%; Pred. No. 3.1e-74;			
175	Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	92 ALYKSXTSNKPLMLIHHLDCEPHSQAULKVFAENKEIQKLAEQFVILNYETTDKHLSP 151	Db				
	61 ALYKSXTSNKPLMLIHHLDCEPHSQAULKVFAENKEIQKLAEQFVILNYETTDKHLSP 120	Qy				
	61 ALYKSXTSNKPLMLIHHLDCEPHSQAULKVFAENKEIQKLAEQFVILNYETTDKHLSP 120	Db				
	152 DGQYPRIMFYDPSLTIVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTEL 206	Qy				
	121 DGQYPRIMFYDPSLTIVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTEL 175	Db				
		RESULT 2				
T31643	hypothetical protein Y57A10A - Caenorhabditis elegans	C;Species: Caenorhabditis elegans	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000			
	R;Smyle, R.	A;Accession: T31643	A;Cross-references: 1-186 <WIL>			
		A;Accession: T31643	A;Experimental source: clone Y57A10A			
		A;Molecule type: DNA	C;Genetics:			

A;Gene: CESP;Y57A10.A.U
 A;Introns: 70/1
 C;Superfamily: human anterior gradient-2

Query Match Score 199; DB 2; Length 186;
 Best Local Similarity 30.0%; Pred. No. 1.1e-10;
 Matches 51; Conservative 38; Mismatches 57; Indels 24; Gaps 6;

Qy 41 LLLVALSYTLARDTIVKPGAKKDKDSRPLPKLQPTLSRGDWGDQLIWTQTYEALYKSFKTSN 100
 Db 4 LLLVAL-----VSAYAYSFEDKIKNSIONPLARGGDDIAWVK-WEDAETALDID 53

Qy 101 KPLMTIHHDECPHQALKKVFAEN--KEIQKLAEQFVFLNLV--YETTDKGHLSPDQY 155
 Db 54 KPIELIHKWSWCHACKLKKTFOQSNAKAFKQKUSEHFLVNTDDEPEEEYRPDKY 113

Qy 156 VPRIMFVDPSTSITVRADITGRYSNRL---YAYEPADTFLLDNMKKAALK 200
 Db 114 IPRLLFLDKN---GDLQEFKNKKAEEYKNAYYSSPADILNSMKDVK 159

RESULT 3

D64900 probable protein disulfide-isomerase (EC 5.3.4.1) MTH1745 [similarity] - Methanobacterium thermoadautotrophicum D69100
 C;Species: Methanobacterium thermoadautotrophicum
 C;Accession: D69100 #sequence_revision 05-Dec-1997 #text_change 15-Sep-2000
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Vicaire, R.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A;Reference number: A63000; MUID:98037514; PMID:9371463
 A;Accession: D69100
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-150 <MTH>
 A;Cross-references: GB:AB000930; GB:AB000666; NID:9222872; PIDN:AAF86215.1; PID:922287
 C;Genetics:
 A;Gene: MTH1745
 C;Keywords: intramolecular oxidoreductase; isomerase

Query Match Score 119; DB 2; Length 150;
 Best Local Similarity 27.1%; Pred. No. 0.0015;
 Matches 35; Conservative 28; Mismatches 46; Indels 20; Gaps 4;

Qy 39 AFLLVALSYTLARDTIVKPGAKKDKDSRPLPKLQPTLSRGDWGDQLIWTQTYEALYKSFKTSN 98
 Db 19 AGLSLVLITYV-----QPRVQSLSTTDEKD-LKWTTEDEAKEASR 60

Qy 99 SNKPLMIHHDECPHQALKKVFAENKEQ-KLAEQFVFLNLVYETTDKGHLSPDQY V 156
 Db 61 TGKNNVFMVFASWCPACQLESETLQNTVEVRRRAEDFTAVKIDVDTSALSSRYTVG 120

Qy 157 PRIMFVDPSTSITVRADITGRYSNRLAYE 184
 Db 320 NGTGTAPSFLSDPSL--ADLDEMRN-YKYE 348

RESULT 5

G72016 probable disulfide bond isomerase - Chlamydophila pneumoniae (strains CWL029 and AR39)
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C;Accession: G72016; B81523
 R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomics of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72000; MUID:9920606; PMID:10123288
 A;Accession: G72016
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-348 <ARN>
 A;Cross-references: GB:AB001673; GB:AE01363; NID:94377252; PIDN:AAD19071.1; PID:9437725
 A;Experiment source: strain CWL029
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.;
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genomic sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:1064935
 A;Accession: B81523
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-348 <REA>
 A;Cross-references: GB:AE002251; GB:AE002251
 A;Experiment source: strain AR39, HL cells
 C;Genetics:
 A;Gene: CPn0933; CP0928

Query Match Score 87; DB 2; Length 348;
 Best Local Similarity 25.0%; Pred. No. 3.5;

RESULT 4

S5919 hypothetical protein YMR191W - Yeast (Saccharomyces cerevisiae)
 N;Alternate name: hypothetical protein YMR646.03
 C;Species: Saccharomyces cerevisiae
 C;Accession: S50919; S55721
 R;Pearson, D.; Bowman, S.
 Submitted to the EMBL Data Library, January 1995
 A;Reference number: S50919
 A;Molecule type: DNA
 A;Residues: 1-458 <PEA>

Sequence										
Matches	29;	Conservative	26;	Mismatches	37;	Indels	24;	Gaps	4;	
Qy	29	RVAMEKIPVSAFLLLVALSYTTLARDTTVKPGAKKDTSRPLKPQTLSRGDQLIWTQT	88							
Db	9	RCSLKQKVLTLL--LSSLSS--PTLEAENRDS-----DSIVWHLDD	46							
Qy	89	YEEALYKSKTSNKPLMIIHHLDEC--PHSQALKVPAENKEIQKLAEQFVLLNLY	142							
Db	47	YQEALOKSKEAELPLLVIFSGSDWNGCMIKIRKEVLESPEPIKRYQGKFVCVEVEY	102							
RESULT 6										
C86607	disulfide bond isomerase [imported] - Chlamydophila pneumoniae (strain J138)									
C;Species: Chlamydophila pneumoniae, Chlamydida pneumoniae										
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001										
Db	C86607	#Accession: C86607								
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is										
Nucleic Acids Res. 28, 2311-2314, 2000										
A;Title: Comparison of whole genome sequences of chlamydial pneumoniae J138.										
A;Reference number: A86491; PMID:20330349; PMID:10871362										
A;Accession: C86607										
A;Molecule type: DNA										
A;Residues: 1-348 <STO>										
A;Cross-references: GB:BA000008; NID:98979307; PID:BA99141.1; GSPDB:GN00142										
A;Experimental source: strain J138										
C;Genetics:										
A;Gene: CPJ0933										
Query Match	8.2%	Score 87;	DB 2;	Length 348;						
Best Local Similarity	25.0%	Pred. No. 3.5;								
Matches	29;	Conservative	26;	Mismatches	37;	Indels	24;	Gaps	4;	
Qy	29	RVAMEKIPVSAFLLLVALSYTTLARDTTVKPGAKKDTSRPLKPQTLSRGDQLIWTQT	88							
Db	9	RCSLKQKVLTLL--LSSLSS--PTLEAENRDS-----DSIVWHLDD	46							
Qy	89	YEEALYKSKTSNKPLMIIHHLDEC--PHSQALKVPAENKEIQKLAEQFVLLNLY	142							
Db	47	YQEALOKSKEAELPLLVIFSGSDWNGCMIKIRKEVLESPEPIKRYQGKFVCVEVEY	102							
RESULT 7										
S19188	myosin-V - chicken calmodulin-binding protein; myosin I heavy chain, 190K									
C;Species: Gallus gallus (chicken)										
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001										
Db	A44359; PMID:9107155; PMID:1469047	#Accession: A44359								
R;Espreaficco, B.M.; Cheney, R.E.; Matteoli, M.; Nascimento, A.A.; De Camilli, P.V.; Lars										
submitted to the EMBL Data Library, February 1992										
A;Description: Complete cDNA coding sequence of chicken brain p190, a calmodulin binding										
A;Accession: S19188										
A;Molecule type: mRNA										
A;Residues: 1-1830 #Accession: BMBL:Z11718										
A;Cross-references: BMBL:Z11718										
A;Cell: Cell Biol. 119, 1541-1557, 1992										
A;Title: Primary structure and cellular localization of chicken brain myosin-V (p190), a										
A;Reference number: A44359; PMID:9107155; PMID:1469047										
A;Accession: A44359										
A;Residues: 1-1688 'R' 1690-1830 <ES2>										
A;Experimental source: brain										
A;Note: Sequence extracted from NCBI backbone (NCBIN:121153, NCBI:IP:121154)										
A;Accession: B44359										
A;Molecule type: protein										
A;Residues: 155-164 <ES3>										
B;Sanderson, G.; Licher, B.; Meyer, H.E.; Kilimann, M.W.										
FEBS Lett. 311, 295-298, 1992										
Qy	192	LDNMWKALKLKT	204							

Db	1112 ADNVEKSAKUQPQT 1124	77 SPPF--EVIBTGNGEFDIMVRIF---PAPAEHKALTFYHILKLHPYGPRLMEMKASGG 130	
RESULT 9			
S51421	hypothetical protein YLR176C - yeast (Saccharomyces cerevisiae)	127 EIQKLAEQFVILLNLVYETTDKHLSP---DQXYVPRIMFVDPSTLVRADITGRYSNRLYA 182	
N;Alternate names: hypothetical protein L9470.18		131 LVE\$QYEBIVFNEPFETYKLU\$QNPIGDGH----GLAVESEPDPHSQQHQ 180	
C;Species: Saccharomyces cerevisiae		183 YEPADTALLDNMKKALKLKTEL 206	
C;Accession: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998		181 DEADKDLFAIQEVKTIEMYKQV 204	
R;Wohldmann, P.			
Submitted to the EMBL Data Library, November 1994		RESULT 11	
A;Description: The sequence of <i>S. cerevisiae</i> cosmid 9470.		C96229 unknown protein F19K16.21 [imported] - <i>Arabidopsis thaliana</i>	
A;Reference number: S51421		C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)	
A;Molecule type: DNA		C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	
A;Residues: 1-771 <WHD>		C;Accession: C96829	
A;Cross-references: EMBL:U17246; NID:9577192; PID:9577210; MIPS:YLR176C		R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.	
C;Genetics:		Nature 408, 816-820, 2000	
A;Gene: SGD:RFX1		A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.-A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	
A;Cross-references: SGD:S0004166; MIPS:YLR176C		A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	
A;Map position: 12R		A;Title: Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis</i> .	
Query Match 7.9% Score 84 DB 2; Length 771;		A;Reference number: A86141; PMID:21016719; PMID:11130712	
Best Local Similarity 25.7% Pred. No. 18;		A;Status: preliminary	
Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;		A;Molecule type: DNA	
Db	8 LSGSGP-----HPSRLTQG----WVRSRVAAMEKIPVSAILLVALSYTAR 52	A;Residues: 1-918 <STO>	
Db	89 LIGSGRGSHKPSPTPTQPAQPATQROPATSYVPPASISUNRSNSAYPLSFKESETLN 148	A;Cross-references: GB:AE005173; NID:96453864; PIDN:AAF0904.1; GSDB:GN00141	
Db	53 D--TTVK-----PGAKEDTKDSRPKLPQTLSRGWGDOLINTQTYBALYKSSTSNSKP 102	C;Genetics:	
Db	149 NPPTAAKRTNTFPSPSSTKQKTSQERISSIRRNTQELAQIAEN--NKSKTIEF 206	A;Gene: F19K16.21	
Db	103 LMIIH-----LDECPSQALKKVFENKEIQKLAEFQFLNLVYETTDKHLSPDGY 155	A;Map position: 1	
Db	207 AQIVKHAETKVLMSMDSQNTSKAALQLAQNRRER--QYFALLMLQNCQSQHDS---Y 260	Query Match 7.9% Score 83.5; DB 2; Length 918;	
Db	156 VPR 158	Best Local Similarity 21.3%; Pred. No. 24;	
Db	261 VPR 263	Matches 46; Conservative 41; Mismatches 76; Indels 53; Gaps 9;	
RESULT 10		Db	149 PQSQRLLBESSEYSLQTPESSGYKTSLOPNEKLEMATSDQSQEOPK--SEABBSQPDS 206
T37559	probable transcription factor - fission yeast (Schizosaccharomyces pombe)	Qy	87 QTVEEALYKSKTSNPKLM---IHHLDCEPHQSQUALKKVFAENKEIQKLAEQVFL---138
C;Species: Schizosaccharomyces pombe		Db	207 EAKEVTEVKNDTVHSPLDGKHITMDETTNEQ---EILGENLEGRSSKKNFEVSPDIN 263
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999		Qy	139 -----NLVYETTDKHLSPDGOVPR-----IMFDPSLTVRADI---172
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.		Db	264 HVNRIESPYAHPLIFESDG---SPYESSIPKRSSSDEISERIVDFVSRIDSRLDTSEL 320
Submitted to the EMBL Data Library, February 1996		Qy	173 --TGRYSNRLYAYEPADTALLDNMKKALKLKTEL 206
A;Accession: T37859		Db	321 NESRSSSATNSDADVILEEKTKEIKMLNAL 356
A;Status: preliminary		RESULT 12	
A;Molecule type: DNA		T40683 cell cycle protein kinase hsk1 - fission yeast (<i>Schizosaccharomyces pombe</i>)	
A;Experimental source: strain 972h-; cosmid c17G8		C;Species: <i>Schizosaccharomyces pombe</i>	
A;Gene: SPDB:SPAC17G8.07		C;Accession: T40683	
C;Genetics:		C;Accession: T40683	
A;Map position: 1		C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000	
Query Match 7.9% Score 83.5; DB 2; Length 217;		R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.	
Best Local Similarity 20.6% Pred. No. 4.1;		Submitted to the EMBL Data Library, January 1999	
Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;		A;Reference number: 221944	
Db	14 HPSRLTQG-----RWVRSRVAAMEKIPVSAILLVALSYTARDITVKGAKDTPKD 66	A;Status: preliminary; translated from GB/EMBL/DDBJ	
Db	39 HTWLIFVEGVGDGEDISKWTR-----VVFKL-----HDIVNNP---TRTE 76	A;Molecule type: DNA	
Qy	67 SRPKLSPQTLSRGWGDOLINTQTYBALYKSSTSNSKPMLM-----IHHLDCEPHQSQUALKKVFAENK 126	A;Cross-references: ENBL:AL035263; PIDN:CA838417.1; GSDB:GN00067; SPDB:SPBC776.12C	
A;Experimental source: strain 972h-; cosmid C776		A;Experimental source: strain 972h-; cosmid C776	

C; Genetics:
 A; Gene: SPBC776.12C
 A; Map position: 2
 C; Introns: 77/1; 92/2; 331/1
 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 Query Match 7.8*; Score 83; DB 2; Length 479;
 Best Local Similarity 22.4%; Pred. No. 12;
 Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;
 A; Best Local Similarity 22.4%; Pred. No. 12;
 A; Molecule type: DNA
 A; Residues: 1-788 <AOF>
 A; Cross-references: GB:AE000748; NID:92983960; PIDN:AA07512.1; PID:92983965; GB:AE00065
 A; Experimental source: strain VFS5
 C; Genes: IPIA
 A; Gene: IPIA
 Query Match 7.8*; Score 82.5; DB 2; Length 788;
 Best Local Similarity 23.0%; Pred. No. 25;
 Matches 49; Conservative 34; Mismatches 73; Indels 57; Gaps 10;
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 A; Molecule type: DNA
 A; Residues: 1-788 <AOF>
 A; Cross-references: GB:AE000748; NID:92983960; PIDN:AA07512.1; PID:92983965; GB:AE00065
 C; Status: preliminary; nucleic acid sequence not shown; translation not shown
 V.; Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov.
 Nature 392, 353-358, 1998
 A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A; Reference number: A70300; MUID:9819666; PMID:9537320
 A; Accession: C70441
 A; Status: preliminary
 A; Molecule type: DNA
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 A; Experimental source: strain VFS5
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 A; Cross-references: Nature 392, 353-358, 1998
 C; Species: Aquifex aeolicus
 C; Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
 R.; Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov.
 V.; Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov.
 Nature 392, 353-358, 1998
 A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A; Reference number: A70300; MUID:9819666; PMID:9537320
 A; Accession: C70441
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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 A; Molecule type: DNA
 A; Residues: 1-788 <AOF>
 A; Cross-references: Nature 392, 353-358, 1998
 C; Species: Schizosaccharomyces pombe
 C; Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999
 C; Accession: S56143; T40682
 R.; Masai, H.; Miyake, T.; Arai, K.
 EMBL J. 14, 3094-3104, 1995
 A; Title: hsk1(+) - Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae
 A; Reference number: S56143; MUID:95347336; PMID:761824
 A; Accession: S56143
 A; Molecule type: DNA
 A; Residues: 1-507 <MAS>
 A; Cross-references: GB:D50493; NID:9807845; PIDN:BAA09087.1; PID:di009722; PID:9807846
 A; Experimental source: strain JY2
 R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutner, M.; Wambutt, R.
 Submitted to the EMBL Data Library, January 1999
 A; Reference number: Z21944
 A; Accession: T40682
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-507 <LN>
 A; Cross-references: EMBL:AL03563; PIDN:CA222885.1; GSPDB:GN00067; SPDB:SPBC776.12C
 A; Experimental source: strain 972h-; cosmid C776
 C; Genetics:
 A; Gene: hsk1; SPBC776.12C
 A; Map position: 2
 A; Intron: 7/1; 359/1
 C; Keywords: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 P; 66-404/Domain: protein kinase homology <KIN>
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 Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;
 A; Best Local Similarity 22.4%; Pred. No. 13;
 A; Molecule type: DNA
 A; Residues: 1-788 <AOF>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:913325078
 R.; Mueller, O.T.; Hartmann, J.K.Jr.; Gallardo, L.A.; Essig, Y.P.; Miller, K.L.; Papenf.
 Am. J. Hum. Genet. 49, 804-810, 1991
 Cell 64, 649-665, 1991
 A; Title: Low oculocerebrorenal syndrome in a female with a balanced X;20 translocation:
 A; Reference number: H59431
 A; Accession: H59431
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-93 <DUD>
 A; Cross-references: GB:NP_001578; PID:913325078; PID:913325070; PID:913325070
 R.; Mueller, O.T.; Hartmann, J.K.Jr.; Gallardo, L.A.; Essig, Y.P.; Miller, K.L.; Papenf.
 Am. J. Hum. Genet. 49, 804-810, 1991
 Cell 64, 649-665, 1991
 A; Title: Low oculocerebrorenal syndrome in a female with a balanced X;20 translocation:
 A; Reference number: H59431
 A; Accession: H59431
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-93 <RUB>
 A; Cross-references: GB:NP_001578; PID:913325078; PID:913325070; PID:913325070
 R.; Attre, O.; Olivos, I.M.; Okabe, I.; Bailey, L.C.; Nelson, D.L.; Lewis, R.A.; McInnes,
 Nature 358, 239-242, 1992
 A; Title: The Lowe's oculocerebrorenal syndrome gene encodes a protein highly homologous
 A; Reference number: A59443; MUID:92334430; PMID:1321346
 A; Accession: A59443
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-93 <ATT>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:913325078
 R.; Attre, O.; Olivos, I.M.; Okabe, I.; Bailey, L.C.; Nelson, D.L.; Lewis, R.A.; McInnes,
 Nature 358, 239-242, 1992
 A; Title: The Lowe's oculocerebrorenal syndrome gene encodes a protein highly homologous
 A; Reference number: A59443; MUID:92334430; PMID:1321346
 A; Accession: A59443
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-93 <ATT>

RESULT 14

R; Beahey, A.M.; Charnas, L.R.; Nussbaum, R.L.
 Hum. Mol. Genet. 2, 461-463, 1993
 A; Title: Nonsense mutations in the OCRL-1 gene in patients with the oculocerebrorenal syndrome
 A; Reference number: B59432; MUID:93278398; PMID:8504307
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-893 <LEA>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:NP_001578.2
 R; Zhang, X.; Jefferson, A.B.; Auehavikat, V.; Majerus, P.W.
 Proc. Natl. Acad. Sci. U.S.A. 92, 4853-4856, 1995
 A; Title: The protein deficient in Lowe syndrome is a phosphatidylinositol-4,5-bisphosphate
 A; Reference number: C59432
 A; Accession: D59432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-893 <ZHA>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:NP_001578.2
 R; Nussbaum, R.L.; Orrison, B.M.; Janne, P.A.; Charnas, L.; Chinault, A.C.
 Hum. Genet. 99, 145-150, 1997
 A; Title: Physical mapping and genomic structure of the Lowe syndrome gene OCRL1.
 A; Reference number: D59432
 A; Accession: D59432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-893 <NUS>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:NP_001578.2
 R; Janne, P.A.; Suchy, S.F.; Bernard, D.; Macdonald, M.; Grinberg, A.; Wynshaw-Brown, C.; Govers, C.; Communi, D.; Pessesse, X.
 J. Clin. Invest. 101, 2042-2053, 1998
 A; Title: Functional overlap between murine Inpp5b and Ocrl1 may explain why deficiency of
 A; Reference number: E59432
 A; Accession: E59432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-893 <JAN>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:NP_001578.2
 R; Ernaut, C.; Biochim. Biophys. Acta 1436 (1-2), 185-199, 1998
 A; Title: The diversity and possible functions of the inositol polyphosphate 5-phosphatas
 A; Reference number: F59432
 A; Accession: F59432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-893 <ERN>
 A; Cross-references: GB:NP_001578; PID:913325070; PID:NP_001578.2

Query Match Score 81.5; DB 2; Length 893;
 Best Local Similarity 7.7%; Pred. No. 36;
 Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;

QY	55	TVKPGAKKDTKDSRPK-LPQTLSRGWMGDOLINTQTYEAL-YKS---KTS-NKPMI	106
Db	476	: : : : : : : : : : : : : : : : : : :	530
QY	107	HHL---DECPhSOALKVFAENKEIQKLA-----QFLILNLVYETTDK-	147
Db	531	: : : : : : : : : : : : : : : : : :	586
QY	148	FHIGVKVVD---RYRKVFEDSYTRIMDRMENDFLPSLERSREFVNPKRQLQEK	586
Db	587	-HLSPDG---YVPRTM-----FVDSLTVRADITGYSNRLYAYE	184
QY	185	PADTAIIIDN 194	185
Db	639	SKDSTVILNS 648	639

Search completed: November 26, 2003, 15:56:25
 Job time : 22 secs

Scoring table:	BLOSUM62					
Searched:	127863 seqs, 47026705 residues					
Total number of hits satisfying chosen parameters:	127863					
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 0%						
Post-processing: Maximum Match 100%						
Database :	SwissProt_41;*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	4.48	XAG_XENLA	42.1	183	1	P58668 xenopus lae
2	437.5	XENLA	41.2	185	1	P5869 xenopus lae
3	224.5	XENLA	21.1	170	1	Q9CQU0 mus musculu
4	222	XENLA	20.9	172	1	Q95881 homo sapien
5	87.5	XENLA	8.2	458	1	P42933 saccharomyces
6	85.5	XENLA	8.0	1829	1	Q02440 gallus gall
7	84	XENLA	7.9	911	1	P48743 saccharomyces
8	83.5	XENLA	7.9	217	1	Q10319 schizosacch
9	83	XENLA	7.8	507	1	P50582 schizosacch
10	81.5	XENLA	7.7	901	1	Q01968 homo sapien
11	81.5	XENLA	7.7	1398	1	P41001 plasmidium
12	80	XENLA	7.5	339	1	P43484 rhodococcus
13	80	XENLA	7.5	843	1	Q05150 saccharomyces
14	79.5	XENLA	7.5	301	1	Q92140 helicobacte
15	79	XENLA	7.4	477	1	Q9YF3 ratmus norv
16	79	XENLA	7.4	510	1	P14003 drosophila
17	78.5	XENLA	7.4	280	1	P54374 bacillus su
18	78.5	XENLA	7.4	917	1	Q49498 arabidopsis
19	78.5	XENLA	7.4	1262	1	Q94514 mus musculu
20	78.5	XENLA	7.4	1828	1	Q9YF3 ratmus norv
21	78	XENLA	7.3	337	1	P14003 drosophila
22	78	XENLA	7.3	887	1	Q63416 ratmus norv
23	78	XENLA	7.3	1853	1	Q95A10 mus musculu
24	78	XENLA	7.3	1855	1	Q9YF3 ratmus norv
25	77	XENLA	7.2	729	1	Q92140 caenorhabdi
26	76.5	XENLA	7.2	524	1	P59385 bradyrhizobium
27	76.5	XENLA	7.2	1025	1	Q03278 nasonia vit
28	76	XENLA	7.1	543	1	P23443 escherichia
29	76	XENLA	7.1	1650	1	P18948 caenorhabdi
30	76	XENLA	7.1	2145	1	Q9u290 caenorhabdi
31	75.5	XENLA	7.1	580	1	Q10769 mycobacteri
32	75.5	XENLA	7.1	2318	1	NTC3_MOUSE
33	75	XENLA	7.1	1694	1	Q62230 mus musculu

ALIGNMENTS

RESULT 1						
XAG_XENLA						
ID XAG_XENLA						
AC P5868;						
STANDARD;						
PRT; 183 AA.						
DT 01-NOV-1997 (Rel. 35, Created)						
DT 01-NOV-1997 (Rel. 35, Last sequence update)						
DT 01-NOV-1997 (Rel. 35, Last annotation update)						
DE Putative secreted protein XAG precursor.						
GN XAG.						
OS Xenopus laevis (African clawed frog).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucoleostomi;						
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;						
OC Xenopodinae; Xenopus.						
NCBI_TaxID=8355;						
RN [1]						
RP SEQUENCE FROM N.A.						
RC TISSUE-Cement gland;						
RX MEDLINE=97003224; PubMed=8850563;						
RA Sive H., Bradley L.;						
RT "A sticky problem: the Xenopus cement gland as a paradigm for anteroposterior patterning.", Dev. Dyn. 205:265-280(1996);						
RL - SUBCELLULAR LOCATION: Secreted (Probable).						
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND.						
CC - SIMILARITY: HIGH, TO XENOPUS NP77.						
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CC DR EMBL; U76752; AAB18819.1; -.						
CC KW Signal.						
FT SIGNAL 1 18 POTENTIAL.						
FT CHAIN 19 183 PUTATIVE SECRETED PROTEIN XAG.						
SQ SEQUENCE 183 AA; 20475 MW; 95E12B06FCB8DC8 CRC64;						
Query Match 42.1%; Score 448; DB 1; Length 183;						
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Qy 39 AFLLLVALSFTYLARDITVVKP--GAKKDTKDSRPIKUP-----QTISRGWGDQLIWTQTY 89						
Db 6 SLVCVLLCSAEGAVLKKPKQAGITDKTDQEPAKTKGLKTDRGWGESIEWVQTY 65						
Qy 90 EEALYKSXTSNKPLMITHHDECPSQALKVFAENKEIQLA-EQFVLNLNVYETTDKH 148						
Db 66 EEGLAKARENKKPLMYTHLEDCPYSTALKFAVADRMQKLAQEDFTIMLNVHPYADEN 125						
Qy 149 LSPDGQYVPRIMEVDFSLTVRDTIERSNRLYAYEPADTALLDNMKKALKLITTEL 206						
Db 126 QSPDGHYVPRVTFIDPSLTVRSDLQKRYGNYMVAADDIPELINTNMKAKSFKLTEL 183						

FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 170 THIOREDOXIN-LIKE PROTEIN P19.
 FT DISULFID 64 67 THIOREDOXIN-ACTIVE (POTENTIAL).
 FT SITE 167 170 PREVENT SECRETION FROM ER (POTENTIAL).
 FT CARBOHYD 128 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 170 AA; 19048 MW; 5B91Fc9BE12C5E4; CRC64;
 Query Match Score 224.5 ; DB 1 ; Length 170 ;
 Best Local Similarity 34.9% ; Pred. No. 6.4e-14 ;
 Matches 58 ; Conservative 25 ; Mismatches 58 ; Gaps 4 ;
 Qy 39 APLLVVLSYLTARDITVKPGAKKDTPKLPQTLRGNDQLIWTQTYBEALYKSTK 98
 Db 14 SFLLITTS-----DGR----TGJGKGFDDHIM-RTLEDGKKEAAA 50
 Qy 99 SNKPLMTHHLDCEPHSQUALKVKFAENKEIQKLAEQFVLLNL--VYETTDKHLSPGQQVY 156
 Db 51 SGLPLMVTHIKSWCGACKALKRKAESTEISPLSHNFMVNLDEEPFRDDEFSPDGYY 110
 Qy 157 PRIMFVDPSLTTRADITGRYSNRLYAYEPADTAFLDNMKKALKL 202
 Db 111 PRILFDLPSKGKVRPELINEGNPSKSYKFVYSAEQVYQGMKEAQERL 156
 Query Match Score 222 ; DB 1 ; Length 172 ;
 Best Local Similarity 34.2% ; Pred. No. 1.1e-13 ;
 Matches 54 ; Conservative 26 ; Mismatches 56 ; Indels 22 ; Gaps 3 ;
 FT CHAIN 27 172 THIOREDOXIN-LIKE PROTEIN P19.
 FT DISULFID 66 69 REDOX-ACTIVE (POTENTIAL).
 FT CONFLICT 102 102 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 172 AA; 3092E9515A7C0494 CRC64 ;
 Qy 107 HHLDECPHSQALKVYKAENKEIQKLAEQFVLLNL--VYETTDKHLSPDQGQYVPRMFVDP 164
 Db 2 ETRPLIGATCLLGFSFLLYLVISSDQHNGLKGKFGDHWH-RTLEDGKKEAAAAGLPLMVI 60
 Qy 107 HHLDECPHSQALKVYKAENKEIQKLAEQFVLLNL--VYETTDKHLSPDQGQYVPRMFVDP 164
 Db 61 IHKSWGACKALKRKAESTEISPLSHNFMVNLDEEPFRDDEFSPDGYYIPRLFLDP 120
 Qy 165 SLTVRADITGRYSNRLYAYEPADTAFLDNMKKALKL 202
 Db 121 SGKVHPPEIINENGNPSPYKPYVSAEQQVQCMKEAQERL 158
 RESULT 4
 ID TL19_HUMAN STANDARD ; PRT; 172 AA.
 AC 09581 ; Q96H50 ;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Thioredoxin-like protein p19 precursor (Endoplasmic reticulum protein
 DB PR19).
 GN Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606 ;
 RN [1]
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 RC TISSUE=Brain;
 RA Mei G., Yu W., Gibbs R.A.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liu F., Rong Y., Zeng L., Qi X., Han Z.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon Kidney, and Ovary;
 RX MEDLINE=22388257; PubMed=1477932;
 RA Strasserberg R.L., Feingold E.B., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeiberger B., Buetow K.H., Schaeter C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Wang S.I., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Smailus D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -!- SIMILARITY: Contains 1 thioredoxin domain.

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 CC DR EMBL ; AF53146 ; AAC34781.1 ;
 CC DR EMBL ; BC001493 ; AAH01493.1 ;
 CC DR EMBL ; BC008953 ; AAH08953.1 ;
 CC DR EMBL ; BC008913 ; AAH08913.1 ;
 CC DR InterPro ; IPRO06662 ; Thioreredoxin.
 CC DR PROSITE ; PS00194 ; THIOREDOXIN_1 ;
 CC KW Endoplasmic reticulum; Redox-active center; signal.
 CC FT SIGNAL 1
 CC FT CHAIN 27 172
 CC FT DISULFID 66 69
 CC FT CONFLICT 102 102 D > H. (In Ref. 3; AAH08913.)
 CC SQ SEQUENCE 172 AA; 3092E9515A7C0494 CRC64 ;
 CC DR PRT; 172 AA ;
 CC DR PROSITE ; PS00194 ; THIOREDOXIN_1 ;
 CC KW Endoplasmic reticulum; Redox-active center; signal.
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 CC SQ SEQUENCE

RESULT 7		RFX1 YEAST		STANDARD;		PRT;		811 AA.	
ID	RFX1	AC	P48743	DT	01-FEB-1996 (Rel. 33, Created)				
AC		DT	15-SEP-2003 (Rel. 42, Last annotation update)						
DB		DB	RFX-1 like DNA-binding protein RFX1.						
GN		OS	RFX1 OR CRT1 OR YLR176C OR L9471.						
		OC	Saccharomyces cerevisiae (Baker's yeast).						
		OC	Bukaryota; Fungi; Ascomycota; Saccharomycetes;						
		OC	Saccharomycetales; Saccharomyctaceae;						
		OC	Saccharomyces; Schizosaccharomycetaceae;						
		OX	NCBI_TaxID=4932;						
RN		[1]							
RP		SEQUENCE FROM N.A.							
RC		STRAIN-S288C / AB972;							
RX		MEDLINE=9731367/; PubMed=9169871;							
RA		Johnston M., Hillier L., Dilius L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koettler P., Louis E.J., Messenguy F., Mewes H.W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi B., Porteille D., Purneille B., Rechmann S., Rieger M., Rinke M., Schatzle M., Scheipers B., Schoeller P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandebriel M., Verhaest P., Vierdella F., Voet M., Volkart G., Zollner J.R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." RL Nature 387:87-90(1997).							
CC		- - SIMILARITY: BELONGS TO THE RFX FAMILY.							
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
DR		EMBL; U17246; AAB67470.1; -							
DR		SGD; S000166; RFX1.							
DR		GO; GO:0005737; C:cytoplasm; IDA.							
DR		GO; GO:0005634; C:nucleus; IDA.							
DR		GO; GO:0000122; P:specific transcriptional repressor activity; IDA.							
DR		InterPro; IPR003150; RFX_DNA_binding.							
DR		Pfam; PF0257; RFX_DNA_binding; 1.							
KW		DNA-binding							
SEQUENCE		811 AA; 90583 MW; 116A8B7DDE4FB0 CRC64;							
SQ		8 LSGSGP-----HPSRLTQGR----WVRSRVAMEKIPNSAFLIVALLYTAR 52							
Db		129 LIGSGEGSHKPSPTPTQPAQATPQRQPATSVYVAPISLNRSNSAYPLSFKSEETLNN 188							
Qy		53 D--TTVYK-							
Db		53 D--TTVYK-----PGAKKDTKDSPRKPLPOTLSRGWDOLIWQTYEALYKSSTSNSNP 102							
Qy		189 NPPTAAKRNTFPSSTSKQKTSQKRISSRNTEIAKQIAEN-NKSKTIEY 246							
Db		103 LMIIHH-----LDECPSQALKVFAENKEIQKLAEQYFLINLYETTDKHLSPDGQY 155							
Qy		247 AQIVKHAIEKYLMSMDSQNTSKRALQAEQRER-QVFALLWMKNCKSQHDS---Y 300							
Qy		156 VPR 158							
Db		301 VPR 303							

RESULT 8
RFX1 YEAST STANDARD; PRT; 811 AA.

AC P48743

DT 01-FEB-1996 (Rel. 33, Created)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DB RFX-1 like DNA-binding protein RFX1.

GN RFX1 OR CRT1 OR YLR176C OR L9471.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Bokaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces; Saccharomyces; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP RN

SEQUENCE FROM N.A.

RC RC

STRAIN-S288C / AB972;

RX RX

MEDLINE=9731367/; PubMed=9169871;

RA RA

Johnston M., Hillier L., Dilius L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koettler P., Louis E.J., Messenguy F., Mewes H.W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi B., Pohl T.M., Porteille D., Purneille B., Rechmann S., Rieger M., Rinke M., Schatzle M., Scheipers B., Schoeller P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandebriel M., Verhaest P., Vierdella F., Voet M., Volkart G., Zollner J.R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." RL Nature 387:87-90(1997).

RA RA

Vierdella F., Voet M., Volkart G., Zollner J.R., Hoheisel J.D.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." RL Nature 387:87-90(1997).

RA RA

CC CC

-|- SIMILARITY: BELONGS TO THE RFX FAMILY.

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CC CC

-|- SIMILARITY: BELONGS TO THE RFX FAMILY.

CC CC

Db	77 SPPF--EVETGNGEFDINMVRIF---FAPEAHKLTYYHKLHHPYCPRMEMKASGG	130	CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions. There are no restrictions on its CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).
Qy	127 EIQQLAEQVFLNLVYETDKHLSP---DGQYVPRIMFVDPSTLTVRADITGRYSNRLYA	182	
Db	131 LVEVSYQEVEENPFEVYKULLSONPIGDGH-----GLAVESPDHFPSQOLEQ	180	
Qy	183 YEPADTALLIDNMCKALKLTKE	206	
Db	181 DEADKLDFAIQEVKTIENIKQQV	204	
RESULT 9			
ID	HSKL1 SCHPO STANDARD;	PRT;	507 AA.
AC	PS0582; 094678;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
HSKL1	OR SPBC776.12C.		
GN	cyclic protein kinase hsk1 (EC 2.7.1.-).		
OS	Schizosaccharomyces pombe (Fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomyces pombe;		
OC	Schizosaccharomyces pombe; Schizosaccharomycetaceae;		
OC	Schizosaccharomyces.		
OX	NCBI_TaxID=4896;		
RN	[1]	SEQUENCE FROM N.A. (ISOFORM LONG).	
RP	SEQUENCE FROM N.Y2;		
RC	STRAIN=972;		
MDLINE=95347336;			
RX	PubMed=7621824;		
RA	Masai H., Miyake T., Arai K.-I.;		
RT	"hsk1", a Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae CDC7, is required for chromosomal replication.",		
RT	EMBO J. 14:3094-3104 (1995).		
RN	[2]	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).	
RC	MDLINE=21848401; PubMed=11859360;		
RX	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hiddleigo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagele K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skalton J., Simmonds M., Squares R., Stevens K., Taylor K., Taylor R.G., Tivey A., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Garmynprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel M., Fuchs M., Fritze B., Holzer B., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedder H., Wambutt R., Burnelle B., Goffeau A., Cadieu E., Draimo S., Gloux S., Leilaire V., Mottier S., Galibert F., Aves S.J., Dreano Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rocher M., Gaillardin C., Taillarda V.A., Garzon A., Thode G., Dominguez A., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.", Nature 415: 871-880 (2002).	10	OCRL_HUMAN STANDARD; PRT; 901 AA.
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel M., Fuchs M., Fritze B., Holzer B., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedder H., Wambutt R., Burnelle B., Goffeau A., Cadieu E., Draimo S., Gloux S., Leilaire V., Mottier S., Galibert F., Aves S.J., Dreano Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rocher M., Gaillardin C., Taillarda V.A., Garzon A., Thode G., Dominguez A., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.", Nature 415: 871-880 (2002).	10	OCRL_HUMAN STANDARD; PRT; 901 AA.
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.", Nature 415: 871-880 (2002).	10	OCRL_HUMAN STANDARD; PRT; 901 AA.
CC	- - FUNCTION: REPLICATION.		
CC	- - ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=Long; Sequence=Display;		
CC	Isoform=Short;		
CC	Isoform=PS0582-2; Sequence=VSP 004863;		
CC	- ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC7		
CC	SUBFAMILY.		
RESULT 10			
ID	OCRL_HUMAN		
AC	Q01568; 060800; Q15681; Q15682; Q9UGGS; Q9UMAS;		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	20-DEC-2003 (Rel. 41, Last annotation update)		
DE	Inositol polyphosphate 5-phosphatase OCRL-1		
DE	oculocerebrorenal syndrome protein.		
GN	OR OCRL1; OR INPPPF.		
OS	Homo sapiens (Human)		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]	SEQUENCE FROM N.A. (ISOFORM B).	
RC	TISSUE=Kidney;		
RX	Medline=92334430; PubMed=1321346;		
RA	Attree O., Olivies I.M., Okabe I., Bailey L.C., Nelson D.L., Lewis R.A., McInnes R.R., Nussbaum R.L.;		
RA	"the Lowe's oculocerebrorenal syndrome gene encodes a protein highly homologous to inositol polyphosphate-5-phosphatase.", Nature 358:239-242 (1992).		
RN	[2]		

SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE=Brain; PubMed=9048911;
MEDLINE=972011067;

RA Nussbaum R.L., Orrison B.M., Janne P.A., Charnas L.R., Chinault A.C.;
"Physical mapping and genomic structure of the Lowe syndrome gene
OCRL1";
RT Hum. Genet. 99:145-150(1997).

RN RP SEQUENCE OF 81-901 FROM N.A. (ISOFORMS A AND B).
RA Pavitt R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
[4]

RN RP SEQUENCE OF 426-501 FROM N.A. (ISOFORM B).
RA Mistry S.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
[5]

RN RP SEQUENCE OF 814-843 FROM N.A.
RX MEDLINE=93278398; PubMed=8304307;

RA Leahy A.M., Charnas L.R., Nussbaum R.L.;
"Nonsense mutations in the OCRL-1 gene in patients with the
oculocerebrorenal syndrome of Lowe.";
RT Hum. Mol. Genet. 2:461-463(1993).

RN RP CHARACTERIZATION
RX MEDLINE=95281554; PubMed=7761412;
RA Zhang X., Jefferson A.B.;
RT "The protein deficient in Lowe syndrome is a
phosphatidylinositol-4,5-bisphosphate 5-phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:4853-4856(1995).
[7]

RN RP CHARACTERIZATION
RX MEDLINE=98104142; PubMed=9430698;
RA Hartz P.A., Philip E., Racusen L.C., Majorus P.W.;
RT "Cell lines from kidney proximal tubules of a patient with Lowe
syndrome lack OCRL1 inositol polyphosphate 5-phosphatase and
accumulate phosphatidylinositol 4,5-bisphosphate.";
RT J. Biol. Chem. 273:1574-1582(1998).
[8]

RN RP VARIANTS LS THR-367 DBL; GLY-451; SER-463 AND ARG-524.
RX MEDLINE=9742912; PubMed=3199559;

RA Lin T., Orrison B.M., Leahy A.-M., Suchy S.F., Bernard D.J.,
Lewis R.A., Nussbaum R.L.;
RT "Spectrum of mutations in the OCRL1 gene in the Lowe oculocerebral
syndrome.";
RL Am. J. Hum. Genet. 60:1384-1388(1997).
[9]

RN RP VARIANTS LS TYR-375; GLN-500; ASP-508 AND CYS-513.
RX MEDLINE=98347141; PubMed=3199529;

RA Lin T., Orrison B.M., Suchy S.F., Lewis R.A., Nussbaum R.L.;
RT "Mutations are not uniformly distributed throughout the OCRL1 gene in
Lowe syndrome patients.";
RL Mol. Genet. Metab. 64:58-61(1998).
[10]

RN RP VARIANTS LS GLN-500 AND GLN-524.
RX MEDLINE=98293952; PubMed=36332163;

RA Kawano T., Indo Y., Nakazato H., Shimadzu M., Matsuda I.;
RT "Oculocerebrorenal syndrome of Lowe: three mutations in the OCRL1 gene
derived from three patients with different phenotypes.";
RL Am. J. Med. Genet. 77:348-355(1998).
[11]

RN RP VARIANT LS ARG-522.
RX MEDLINE=99002770; PubMed=9787721; ASP-424 AND TYR-498.

RA Kubota T., Sakurai A., Arakawa K., Shimazu M., Wakui K., Furukata K.,
Fukushima Y.;
RT "Identification of two novel" mutations in the OCRL1 gene in Japanese
families with "Lowe syndrome";
RT Clin. Genet. 54:199-202(1998).
[12]

RN RP VARIANTS LS GLU-357; GLU-421; ASP-424 AND TYR-498.
RX MEDLINE=20382695; PubMed=10923037;

RA Monnier N., Satre V., Lerouge E., Berthoin F., Lunardi J.;
RT "OCRL1 mutation analysis in French Lowe syndrome patients:
implications for molecular diagnosis strategy and genetic

RT counseling.";
RC TISSUE=Brain; PubMed=9048911;
RN RT VARIANTS LS PRO-337 AND GLY-372.
RN RP VARIANT LS PRO-337 AND GLY-372.
RX MEDLINE=20232168; PubMed=10767176;

RA Roschinger W., Muntau A.C., Rudolph G., Roscher A.A.,
Kammerer S.;
RT "Carrier assessment and families with Lowe oculocerebral syndrome:
novel mutations in the OCRL1 gene and correlation of direct DNA
nucleotide mutations in the OCRL1 gene and correlation of direct DNA
novel mutations in the OCRL1 gene and correlation of direct DNA
novel mutations in the OCRL1 gene and correlation of direct DNA
RT diagnosis with ocular examination.";
RL Mol. Genet. Metab. 63:213-222(2000).

CC -1- FUNCTION: Converts phosphatidylinositol 4-phosphate to
phosphatidylinositol 4-phosphate. Also converts inositol 1,4,5-
trisphosphate to inositol 1,4-bisphosphate and inositol 1,3,4,5-
tetraakisphosphate to inositol 1,3,4-trisphosphate. May function in
lysosomal membrane trafficking by regulating the specific pool of
phosphatidylinositol 4,5-bisphosphate that is associated with
lysosomes.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidylinositol 4,5-bisphosphate
bisphosphate + H(2)O = 1-phosphatidylinositol 4-myo-inositol 4-phosphate
+ phosphate

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
Name=A;
CC IsoID=Q01968-1; Sequence=Displayed;
Name=B;
CC IsoID=Q01968-2; Sequence=VSP_002681;

CC -1- TISSUE SPECIFICITY: BRAIN, SKELETAL MUSCLE, HEART, KIDNEY, LUNG,
PLACENTA, AND FIBROBLASTS.

CC -1- DISEASE: DEFECTS IN OCRL ARE THE CAUSE OF LOWE'S OCULOCEREBORENAL
SYNDROME, A DISEASE CHARACTERIZED BY HYDROPHOTHALMIA, CATARACT,
MENTAL RETARDATION, VITAMIN D-RESISTANT RICKETS, AMINOACIDURIA,
AND REDUCED AMMONIA PRODUCTION BY THE KIDNEY

CC -1- SIMILARITY: BELONGS TO THE INOSITOL-1,4,5-TRISPHOSPHATE 5-
PHOSPHATASE TYPE II FAMILY.

CC -1- SIMILARITY: Contains 1 Rho-GAP domain.

CC -1- DATABASE: NAME=Lowe Syndrome mutation database;
WWW="http://research.nhgri.nih.gov/Lowe/".

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CC or send an email to license@isb-sib.ch).

CC DR M88162; AAA59364-1; ALT_INIT.
DR EMBL; U57627; AAB03839-2; -.

CC DR AL022162; CAA18150-1; -.
DR EMBL; AL022162; CAA18151-1; -.

CC DR S62085; AAB26326-1; -.
DR PIR; S29069; S29069.

CC DR Genew; HGNC:8108; OCRL.
DR MIM: 309000;
DR GO; GO:0005795; C:Golgi stack; TAS.
DR GO; GO:0005798; C:Golgi vesicle; TAS.
DR SMART; SM00128; IPPC; 1.
DR SMART; SM0324; RhogAP; 1.
DR PROSITE; PS50238; P:Lipid metabolism; TAS.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPPC.
DR Pfam; PF03177; Exo_endo_Phosph; 1.
DR PF00620; RhogAP; 1.
DR SMART; SM00439; F:Proteins involved in endocytosis; TAS.
DR GO; GO:0006629; P:Lipid metabolism; TAS.
DR InterPro; IPR000300; IPPC.
DR GO; GO:0005795; C:Golgi stack; TAS.
DR GO; GO:0005798; C:Golgi vesicle; TAS.
DR SMART; SM00128; IPPC; 1.
DR SMART; SM0324; RhogAP; 1.
DR PROSITE; PS50238; RHOGAP; 1.
DR Hydrolase; Alternative splicing; Disease mutation.
PT DOMAIN; 721 901
PT VASPIC 707 714
FT /FT1=VSP_002681.
R -> P (IN LOWE SYNDROME).

OX NCBI_TaxID=1833;
 RN [1] SEQUENCE FROM N.A.
 STRAIN NI86/21;
 RX MEDLINE=96082876; PubMed=7583123;
 RA Tamura T., Nagy I., Lupas A., Lottspeich F., Cejka Z., Schoofs G.,
 RA Tanaka K., de Mot R., Baumeister W.;
 RT "The first characterization of a eubacterial proteasome: the 20S complex of Rhodococcus.";
 RT Curr. Biol. 5:766-774 (1995).
 RN [2]
 RP SEQUENCE OF 1-333 FROM N.A.
 STRAIN NI86/21;
 RX MEDLINE=95138028; PubMed=7836301;
 RA Nagy I., Schoofs G., Compereolle F., Proost P., Vanderleyden J.,
 de Mot R.;
 RT "Degradation of the thiocarbamate herbicide EPTC (S-ethyl dipropylcarbamothioate) and biosafening by Rhodococcus sp. strain RT86/21 involve an inducible cytochrome P-450 system and aldehyde dehydrogenase."; J. Bacteriol. 177:676-687 (1995).
 CC -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2097C AND M.LEPRAE
 MLCB2533.24.
 CC ---
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 RL EMBL; U26421; AAC45738.1; -
 DR EMBL; U17130; AAC45747.1; -
 InterPro; IPR004347; DUP245;
 PFam; PF03136; DUF245; 1.
 Hypothetical protein.
 SQ SEQUENCE 339 AA; 37462 MW; 23CB953F88739599; CRC64;
 Query Match 7.5%; Score 80; DB 1; Length 339;
 Best Local Similarity 29.5%; Pred. No. 4.9.;
 Matches 31; Conservative 20; Mismatches 36; Indels 18; Gaps 5;
 AC Q05050;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DB Hypothetical 93.3 kDa protein in TAP42-cyk2 intergenic region.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S28C / AB972;
 RX PubMed=916872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moulie S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;

RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII.";
 RL Nature 387:90-93 (1997);
 CC -!- SIMILARITY: TO YEAST YKL050C.
 CC ---
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 CC ---
 DR EMBL; Z49213; CAA89146.1; -
 DR PIR; S53947; S53947.
 DR SGD; S0004633; YMRO31C.
 KW Hypothetical protein.
 SQ SEQUENCE 843 AA; 93345 MW; 0068D65A229B941D CRC64;
 Query Match 7.5%; Score 80; DB 1; Length 843;
 Best Local Similarity 21.3%; Pred. No. 16;
 Matches 38; Conservative 29; Mismatches 57; Indels 54; Gaps 7;
 AC Q07100;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DB 453 TANRHOEKTSQEIKIKAS-EDALIARMDTKVAERETLLEDTKSKEIEFKKKQMOELKDB 511
 DR RPKLPQTLSREWGDDQLIWTOQYEEALKYSKTSNKLIMITHLDECPSQALKKVAE--- 124
 DR 512 KARLDODLEE-----WGRKCEQDITEARKEOBELLKPYH-DDLANAEAHKTLVEERD 563
 DR 125 --NKELOKLAQFOV-----LLNL--VYETTDKHISPD 152
 DR 564 EINAEITSRLQDAIVDHKRKTSGYGNLDQAKRNTREDDKLLEGOTKESHLND 621
 DR ---
 RESULT 14
 ERA_HELP
 ID ERA_HELPJ
 STANDARD:
 PRT:
 PRY:
 AC Q9Z2M0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DB GTP-binding protein era homolog.
 GN ERA OR JHP0466.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Helicobacteraceae; Helicobacter.
 OC Helicobacter; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OX NCBITaxID=859363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95120557; PubMed=99221682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., de Jonge B.L., Carmel G., Tummillo P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Meberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
 RA ---
 RT "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."
 RL Nature 397:176-180 (1999).
 CC -!- FUNCTION: BINDS BOTH GDP AND GTP, HAS AN INTRINSIC GTPASE ACTIVITY AND IS ESSENTIAL FOR CELL GROWTH (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding proteins. Era subfamily.
 CC -!- SIMILARITY: Contains 1 KH type-2 domain.
 CC ---
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 CC ---

CC EMBL; AE001480; APD06035.1; -.
 DR PIR; G71929; G71929.
 DR HSDB; PG0616; 1EGA.
 DR HAMAP; MF_003467; -; 1ra.
 DR InterPro; IPR005622; Era.
 DR InterPro; IPR040488; KH_dom.
 DR InterPro; IPR004044; KH_TYPE_2.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00013; KH_1.
 DR TIGRFAMS; TIGR00416; era; 1.
 DR TIGRFAMS; TIGR00211; small_GTP; 1.
 DR PROSITE; PS50803; KH_TYPE_2; 1.
 KW GTP-BINDING; RNA-binding; Complete proteome.
 FT NP_BIND 12 19 GTP (POTENTIAL).
 FT NP_BIND 64 68 GTP (POTENTIAL).
 FT NP_BIND 122 125 GTP (POTENTIAL).
 FT DOMAIN 204 280 KH_TYPE_2.
 SQ SEQUENCE 301 AA; 34485 MW; F668C730882EDBF CRC64;

Query Match 7.5%; Score 79.5; DB 1; Length 301;
 Best Local Similarity 27.8%; Pred. No. 4.7; Indels 19; Gaps 4;
 Matches 25; Conservative 13; Mismatches 33;

Qy 89 YEBALYKSTSNSNKP-LMITHHLDPCPHSALKVFAENKEIQKLAEQFVLT----- 137
 Db 106 YEEFL--SUCQKPHILASQKIDTATHQYLOKU-----QEYQKSSSQFIALVPLSAKKSQ 158

Qy 138 -LNUVYETTDKHLSPGDQTVPRIMFVDPSEL 166
 Db 159 NLNALLEC1SKHLSPSAWLFEDLMSDERM 188

RESULT 15
 TFB1_SCBPO STANDARD; PRT; 477 AA.
 AC O12745;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DB Putative RNA polymerase II transcription factor TFIH subunit 1.
 GN SPC16E8.11C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Schizosaccharomyces; Ascomycota; Schizosaccharomycetidae;
 OC Schizosaccharomyces.
 NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hiddle J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Pearson D., Quail M.A., Rabinowitzch E.,
 RA Oliver K., O'Neil S., Saunders D., Seeger K., Sharp S.,
 RA Rutherford K., Butter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Hert R., Robben J., Gymonprez B.,
 RA Weltjens I., Vanscreets E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedder B., Burnelle B.,
 RA Goiffau A., Cadieu E., Dreano S., Gloux S., Lealaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito S.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Supakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The Genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880 (2002).
 CC -!- FUNCTION: Component of the core-TFIH basal transcription factor
 CC -!- (Potential).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 2 BSD domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to licenses@ebi-sib.ch).
 CC EMBL: Z98529; CAB11039.1; -.
 DR PIR; T37791; T37791.
 DR Genedb; SPombe; SPAC16E8.11c; -.
 DR InterPro; IPR005607; BSD.
 DR Pfam; PF03909; BSD; 2.
 DR PROSITE; PS50858; BSD; 2.
 DR Hypothetical protein; Transcription regulation; Nuclear protein;
 DR Repeat.
 FT DOMAIN 60 113 BSD 1.
 FT DOMAIN 134 185 BSD 2.
 SQ SEQUENCE 477 AA; 54558 MW; E21CCP7EC370C34C CRC64;
 SQ Best Local Similarity 26.3%; Prod. No. 9.5;
 SQ Matches 36; Conservative 21; Mismatches 42; Indels 38; Gaps 8;

Query Match 7.4%; Score 79; DB 1; Length 477;
 Best Local Similarity 26.3%; Prod. No. 9.5;
 Matches 36; Conservative 21; Mismatches 42; Indels 38; Gaps 8;

Qy 87 QTYBEALXKSXTSNKP-----IMIITHHLDDEC---PHS-QALK-----KVFAEN 125
 Db 85 QTPEKEAVMKGLHSNEQFWSTRHLRAVERSQQRGFYNVLSTIKPTKTVDSLTVRADITGRYSNRKVAY 144

Qy 126 KEIQLKABQFVLLNLYETTDKHLSP-----DGQVVPIMFVDPSELTKHLSP-----RTTPM 183
 Db 145 QQIHDMFIOQHPLRKVY--DGKVPVPLAEGEFMSRFFPLSKLCKLRGD-----RTTPM 194

Qy 184 EPADTALLDNDNMKALK 200
 Db 195 DPSS-----DIMDKYLK 206

Search completed: November 26, 2003, 15:55:04
 Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:52:23 ; Search time 35 Seconds

(without alignments)
1518.824 Million cell updates/sec

Title: US-09-674-266A-181

Perfect score: 1063
Sequence: RLSSAGTISGSGPHPSRRLT.....DTALLDNMKKALKLKTBL 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SPTRMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

RESULT 1

095994

PRELIMINARY;

PRT; 175 AA.

ID 095994;

AC 095994;

DT 01-MAY-1999

(TREMBLrel. 10, Created)

DT 01-MAY-1999

(TREMBLrel. 10, Last sequence update)

DT 01-OCT-2002

(TREMBLrel. 22, Last annotation update)

DB Secreted CEMENT gland protein XAG-2 homolog (Anterior GRADIENT 2

DB (XENOPUS LAEVIS) homolog (XAG-2 homolog long protein).

GN HAG-2/R OR HAG-2/C OR HPC8.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Breast;

RX MEDLINE=93009231; PubMed=9790916;

RA Thompson D.A.; Weigel R.J.;

RT "HAG-2, the human homolog of the Xenopus laevis cement gland gene

XAG-2, is coexpressed with estrogen receptor in breast cancer cell

RT lines.";

RT Biochem. Biophys. Res. Commun. 251:111-116(1998).

RN [2]

SEQUENCE FROM N.A.

RP Zhang J.S., Smith D.I.;

RA "Human homolog of XAG is differentially expressed in tumors.";

RT Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

RN [3]

RN SEQUENCE FROM N.A.

RC TISSUE=Colon;

RA Strauberg R.;

RT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Zhang J.S., Smith D.I.;

RT "Identification of human homolog of XAG-2 over-expressed in tumors.";

RT Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF038451; AAC82614.1; -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	899	84.6	175	4	095994	095994 homo sapien	O95994 homo sapien
2	828	77.9	175	11	Q88312	Q88312 mus musculu	Q88312 mus musculu
3	555	52.2	165	11	Q8r3w7	Q8r3w7 mus musculu	Q8r3w7 mus musculu
4	555	52.2	166	4	Q8td06	Q8td06 homo sapien	Q8td06 homo sapien
5	550	51.7	165	11	QBBW95	QBBW95 mus musculu	QBBW95 mus musculu
6	548	51.6	159	13	Q9y05	Q9y05 xenopus lae	Q9y05 xenopus lae
7	447	42.1	185	13	Q42251	Q42251 xenopus lae	Q42251 xenopus lae
8	227	21.4	172	4	Q8EH50	Q8EH50 homo sapien	Q8EH50 homo sapien
9	224.5	21.1	170	11	Q9CQU0	Q9CQU0 homo sapien	Q9CQU0 homo sapien
10	222	20.9	172	4	Q95881	Q95881 homo sapien	Q95881 homo sapien
11	199	18.7	186	5	Q3NA78	Q3NA78 caenorhabdi	Q3NA78 caenorhabdi
12	165	15.5	257	5	Q9NS57	Q9NS57 caenorhabdi	Q9NS57 caenorhabdi
13	119	11.2	150	17	Q27777	Q27777 methanobact	Q27777 methanobact
14	113.5	10.7	357	16	Q8EXX9	Q8EXX9 leptospira	Q8EXX9 leptospira
15	89	8.4	950	11	Q924S5	Q924S5 rattus norv	Q924S5 rattus norv
16	88.5	8.3	737	2	Q3AF04	Q3AF04 frankia sp.	Q3AF04 frankia sp.

DR EMBL; AF007791; AAC7358.1;	RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
DR EMBL; BC015503; AAH15503.1;	RA
DR EMBL; AF115926; AAU54870.1;	RA
GENE; HGNC:328; AGR2.	RT
SEQUENCE 175 AA; 19979 MW; F271B1BD377BEE11 CRC64;	RN
Query Match 84.6%; Score 899; DB 4; Length 175;	RN
Best Local Similarity 100.0%; Pred. No. 1.9e-80; Gaps 0;	RP
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE FROM N.A.
32 MEKIPVSAFLLVAVSYTLLARDTIVKGAKKDTSRPLKPTOLSRGHDQLIWTOQYEE 91	RC Tissue-Colon;
1 MEKIPVSAFLLVAVSYTLLARDTIVKGAKKDTSRPLKPTOLSRGNDQLIWTOQYEE 60	RA Strauberg R.; Submitted (AGU-2001) to the EMBL/GenBank/DBJ databases.
92 ALYKSRTSNPKPLMTIHLIDCPSOALKVFAENKEIQGLAEQFVLLNLYVETTDKHLSP 151	DR EMBL; AB016392; BAA32044.1; -
61 ALYKSRTSNPKPLMIIHLIDCPSOALKVFAENKEIQGLAEQFVLLNLYVETTDKHLSP 120	DR EMBL; AF044282; AAC72705.1; -
152 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 206	DR EMBL; AK007677; BAB25181.1; -
121 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 175	DR EMBL; BC013334; AAH13334.1; -
RESULT 2	DR MGD; MGJ:134405; Agric. SQ SEQUENCE 175 AA; 19920 MW; ACC3CF4298668CA CRC64;
O88312 PRELIMINARY; PRT; 175 AA.	DR
ID O88312; PRELIMINARY; PRT; 175 AA.	DR
AC 088312; PRELIMINARY; PRT; 175 AA.	DR
DT 01-NOV-1998 (TREMBUREL. 08, Created)	DR
DT 01-NOV-1998 (TREMBUREL. 08, List sequence update)	DR
DT 01-DEC-2001 (TREMBUREL. 19, Last annotation update)	DR
GOB-4 protein (Anterior GRADIENT 2) (XENOPUS DE LAEVIS)	DR
AGR2 OR GOB-4 OR MAG-2.	DR
Mus musculus (Mouse)	DR
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090; PN [1]	DR
SEQUENCE FROM N.A.	DR
STRAIN=SWISS WEBSTER; MEDLINE=9009231; PubMed=9790916;	DR
RX Thompson D.A., Wiegel R.J.; RT "Cloning of a gene, gob-4, which is expressed in intestinal goblet cells in mice," RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	DR
RN [2]	DR
SEQUENCE FROM N.A.	DR
STRAIN=SWISS WEBSTER; MEDLINE=9009231; PubMed=9790916;	DR
RA Thompson D.A., Wiegel R.J.; RT "Cloning of a gene, gob-4, which is expressed in intestinal goblet cells in mice," RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	DR
RX Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kirosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Asburner M., Baralov S., Casavant T., RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matuo T., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hane D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mastina J., Mazzarelli J., Mombarta P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaki H., Sato K., Schoenbach C., Seya T., Shikata Y., Storch K.-F.,	DR
RC CS7BL/6J; TISSUE=Pancreas; MEDLINE=11085660; PubMed=11217851; RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kirosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matuo T., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hane D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mastina J., Mazzarelli J., Mombarta P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaki H., Sato K., Schoenbach C., Seya T., Shikata Y., Storch K.-F.,	DR
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).	DR
RA Genew; HGNC:328; AGR2.	RT
SEQUENCE 175 AA; 19979 MW; F271B1BD377BEE11 CRC64;	RN
Query Match 84.6%; Score 899; DB 4; Length 175;	RN
Best Local Similarity 100.0%; Pred. No. 1.9e-80; Gaps 0;	RP
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE FROM N.A.
32 MEKIPVSAFLLVAVSYTLLARDTIVKGAKKDTSRPLKPTOLSRGHDQLIWTOQYEE 91	RC Tissue-Colon;
61 ALYKSRTSNPKPLMIIHLIDCPSOALKVFAENKEIQGLAEQFVLLNLYVETTDKHLSP 120	RA Strauberg R.; Submitted (AGU-2001) to the EMBL/GenBank/DBJ databases.
152 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 206	DR EMBL; AB016392; BAA32044.1; -
121 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 175	DR EMBL; AF044282; AAC72705.1; -
RESULT 3	DR EMBL; AK007677; BAB25181.1; -
O88312 PRELIMINARY; PRT; 175 AA.	DR
ID O88312; PRELIMINARY; PRT; 175 AA.	DR
AC 088312; PRELIMINARY; PRT; 175 AA.	DR
DT 01-JUN-2002 (TREMBUREL. 21, Created)	DR
DT 01-JUN-2002 (TREMBUREL. 21, Last sequence update)	DR
DT 01-JUN-2002 (TREMBUREL. 21, Last annotation update)	DR
GOB-4 protein (Anterior GRADIENT 2) (XENOPUS DE LAEVIS)	DR
AGR2 OR GOB-4 OR MAG-2.	DR
Mus musculus (Mouse)	DR
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090; PN [1]	DR
SEQUENCE FROM N.A.	DR
STRAIN=SWISS WEBSTER; MEDLINE=9009231; PubMed=9790916;	DR
RA Thompson D.A., Wiegel R.J.; RT "Cloning of a gene, gob-4, which is expressed in intestinal goblet cells in mice," RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	DR
RX Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kirosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matuo T., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hane D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mastina J., Mazzarelli J., Mombarta P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaki H., Sato K., Schoenbach C., Seya T., Shikata Y., Storch K.-F.,	DR
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).	DR
RA Genew; HGNC:328; AGR2.	RT
SEQUENCE 175 AA; 19979 MW; F271B1BD377BEE11 CRC64;	RN
Query Match 84.6%; Score 899; DB 4; Length 175;	RN
Best Local Similarity 91.4%; Pred. No. 1.3e-73; Gaps 0;	RP
Matches 160; Conservative 8; Mismatches 7; Indels 0; Gaps 0;	SEQUENCE FROM N.A.
92 ALYKSRTSNPKPLMTIHLIDCPSOALKVFAENKEIQGLAEQFVLLNLYVETTDKHLSP 151	RC Tissue-Colon;
61 ALYKSRTSNPKPLMIIHLIDCPSOALKVFAENKEIQGLAEQFVLLNLYVETTDKHLSP 120	RA Strauberg R.; Submitted (AGU-2001) to the EMBL/GenBank/DBJ databases.
152 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 206	DR EMBL; AB016392; BAA32044.1; -
121 DGQYPRIMFVDPSSLTVRADITIGRYSNRLAYAEPADTALLDNMKALKLKTEL 175	DR EMBL; AF044282; AAC72705.1; -
RESULT 4	DR EMBL; BC023499; AAH23499.1; -
O87D06 PRELIMINARY; PRT; 166 AA.	DR
ID Q87D06 PRELIMINARY; PRT; 166 AA.	DR

AC Q8TD06; DT 01-JUN-2002 (TREMBLrel. 21, Created); DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update); OS Homo sapiens (Human). DE Anterior gradient protein 3. OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9606; RN [1]; RP SEQUENCE FROM N.A.; RA Adam P.J., Boyd R., Fletcher G.C., Tyson K., Terrett J.; RT "Proteomic Characterization of Breast Cancer Cell Membranes." ; RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases. DR EMBL; AY069377; AAL5502; 1; -.

SQ SEQUENCE 166 AA; 19171 MW; B1A404BA7705D65 CRC64;

Query Match 52.2%; Score 55; DB 4; Length 166; Best Local Similarity 64.7%; Pred. No. 1.2e-46; Matches 108; Conservative 28; Mismatches 19; Indels 12; Gaps 4;

Db 11 LLLTVTVSNLA-IAIK-----KEKRP--POTLSRGWGDITWQTYEGLFYAQSK 59

Qy 41 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 159

Db 60 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 119

Qy 101 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 159

Db 160 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 206

Qy 160 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 206

Db 120 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLQSEL 166

RESUL T 5

Q8BW95 ID Q8BW95 PRELIMINARY; PRT; 165 AA.

AC Q8BW95 DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DB weakly similar to secreted CEMENT gland protein XAG-2 homolog.

OS Mus musculus (Mouse).

OC Mammalia; Buteraria; Chordata; Rodentia; sciurognathi; Muridae; Murinae; Mus.

NCBI_TAXID=10090; RN [1]; RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6J; TISSUE=Lung; MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; RT EMBL; AK053177; BAC35297.1; -.

SQ SEQUENCE 165 AA; 19139 MW; 243BC7D9A27A173D CRC64;

Query Match 51.7%; Score 550; DB 11; Length 165; Best Local Similarity 63.5%; Pred. No. 3.8e-16; Matches 106; Conservative 28; Mismatches 21; Indels 12; Gaps 4;

Db 10 LLLTVTVSNLA-IAIK-----KEKRP--POTLSRGWGDITWQTYEGLFYAQSK 58

Qy 101 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 159

Db 59 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 118

Qy 160 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 206

Db 119 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLQSEL 165

RESULT 6

Q9OY05 ID Q9OY05 PRELIMINARY; PRT; 159 AA.

AC Q9OY05 DT 01-DEC-2001 (TREMBLrel. 19, Created); DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE Cement gland-specific protein CGS.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; OX Xenopodinae; Xenopus. NCBI_TaxID=8355; RN [1]; RP SEQUENCE FROM N.A.

RA Alexandra E.M., Novoselov V.V., Zaraisky A.G.; RT "Three novel genes expressed in the anterior part of the Xenopus laevis embryo." ; RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases. DR EMBL; AF314056; AAL26844; 1; -.

SQ SEQUENCE 159 AA; 18275 MW; 73BD622848388BBB CRC64;

Query Match 51.6%; Score 548; DB 13; Length 159; Best Local Similarity 60.0%; Pred. No. 5.7e-46; Matches 105; Conservative 26; Mismatches 28; Indels 16; Gaps 1;

Qy 32 MEKIPVYSAFLLVAVASYTLLARDTTVKGAKKDTKDSRKPQTLSGWGDLIWWTQTYEE 91

Db 1 METVLSLFFLIVATSTFLAKE-----RKEPOTLSRGWGNLJEWWTQTYEE 44

Qy 92 ALYKSXTSNKPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 151

Db 45 GLPKAKSENKPILLINHRNDPFSQALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 104

Qy 152 DGQYVPRIMFYDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 206

Db 105 DGQYVPRIMFYDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 159

RESULT 7

O42251 ID O42251 PRELIMINARY; PRT; 185 AA.

AC O42251; DT 01-JAN-1998 (TREMBLrel. 05, Created); DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DB weakly similar to secreted CEMENT gland protein XAG-2 homolog.

OC Mammalia; Buteraria; Chordata; Rodentia; sciurognathi; Muridae; Murinae; Mus.

NCBI_TAXID=10090; RN [1]; RP SEQUENCE FROM N.A.

RX Sive H.L., Hattori K., Weintraub H.; MEDLINE=89324051; PubMed=2752418; RA Sive H.L., Hattori K., Weintraub H.; RT "Progressive determination during formation of the anteroposterior axis in Xenopus laevis." ; RL Cell 58:171-180 (1989).

Qy 41 LLLTVTVSNLA-IAIK-----KEKRP--POTLSRGWGDITWQTYEGLFYAQSK 58

Db 10 LLLTVTVSNLA-IAIK-----KEKRP--POTLSRGWGDITWQTYEGLFYAQSK 58

Qy 101 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 159

Db 59 KPLMIHHLDECPSHQSOALKVPAENKEIQLAE-QFVLLNLVETTDKHISPDGQVPR 118

Qy 160 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLKT 206

Db 119 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLQSEL 165

Query Match 42.1%; Score 447; DB 13; Length 185; Best Local Similarity 50.6%; Pred. No. 6.2e-36;

RP	SEQUENCE FROM N.A.	186 AA;	21467 MW;	F94E13D2F773321E CRC64;
RX	MEDLINE:97261341; PubMed=9110174;			
RA	Yu W.; Anderson B.; Worley K.C.; Murzny D.M.; Ding Y.; Liu W.,			
RA	Riccafrante J.Y.; Wentland M.A.; Lennon G.; Gibbs R.A.;			
RT	"Large-scale concomitant cDNA sequencing.";			
RL	Genome Res. 7:353-358(1997).			
[3]				
RP	SEQUENCE FROM N.A.			
RA	Mei G.; Yu W.; Gibbs R.A.;			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.			
[4]				
RP	SEQUENCE FROM N.A.			
RC	Tissue-Colon, and Kidney;			
RA	Straussberg R.;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.			
[5]				
RP	SEQUENCE FROM N.A.			
RA	Liu F.; Rong Y.; Zeng L.; Qi X.; Han Z.;			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AF131258; ADD20035.1;			
DR	EMBL; EC001493; AAH01493.1;			
DR	EMBL; EC000853; FAH00853.1;			
DR	EMBL; AF543416; DAN34181.1;			
DR	InterPro; IPR006662; Thiorodox_dom2.			
DR	InterPro; IPR006663; Thiorodox_dom2.			
DR	PROSITE; PS00194; THIOREDOKIN_1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 172 AA; 19206 MW;	3092E0515ATC4094 CRC64;		
Query Match	Score 222;	DB 4;	Length 172;	
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Matches	34.2%;	Pred. No. 7	8e-14;	
Qy	66 DSSPKLPQT-----LSRGWGDOLIWTOOTYEALYKSITSNKPKMLI 106			
Db	2 ETRPLRGLTCLGQSFLLVISDGHNGLGKGRGDHTW-RTELDGKREAAASGLPIMVI 60			
Qy	107 HHDELCPHSQALKVPAENKEIQLAEOFVLNL--VETTDKHLSPDQYPRIMVDP 164			
Db	61 ITRKSWCGACKLKPKAESTESELNSHFMVNLEDSEPKQEDFSPDDGGVTPRILFLDP 120			
Qy	165 SLTVRADITGRYSNRLYAYEPADTLLDNMKKALL 202			
Db	121 SGKVHPETINENGNPSTYFYVSQAQVYQGMKEAQERL 158			
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DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
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GN	Y57A10_23.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Peioderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
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RA	Smee R.;			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.			
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RT	"The sequence of C. elegans cosmid F49H12." J. Mol. Biol. 282:2012-2018(1998).			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
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RA	None;			
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RT	"The sequence of C. elegans cosmid F49H12." J. Mol. Biol. 282:2012-2018(1998).			
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DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)		
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GN MTHI745		
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NCBI_TaxID=187420;		
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RA Smith D.R., Doucette-Stamm L.A., DeLoachery C., Lee H.-M., Dubois J., Aldredge T., Bashirraideh R., Blakely D., Cook J., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete Genome sequence of Methanobacterium thermoautotrophicum deltaH: Functional analysis and comparative genomics.", J. Bacteriol. 179:2135-2155 (1997).	RESULT 15	
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DR Pfam; PF0085; thioredox_1.		AC 01-DEC-2001 (TREMBrel. 19, Last sequence update)
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Db 61 TGKNVEMVFSASWCACQKLESETLQNTVEQRRLAEDFIAVKIDVDTSPALSSRYRIVG 120		AC RN [1]
Qy 157 PRIMEVDP\$ 165		AC DR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
Db 121 PTVIILDPS 129		AC CC 1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
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Qy		AC DR InterPro; IPR003111; LON.
Db		AC DR InterPro; IPR001884; Lon_endopep.
Qy		AC DR InterPro; IPR004815; Lon_fam.
Db		AC DR PFM00004; AAA; 1.
Qy		AC DR PFM02130; LON; 1.
Db		AC DR PRINTS; PR00310; CLIPROTEASEA.
Qy		AC DR SMART; SM00382; AAA; 1.
Db		AC DR SMART; SM00464; LON; 1.
Qy		AC DR TIGRFAMs; TIGR00163; lon; 1.
Db		AC DR PROSITE; PS01046; LON SER; 1.
Qy		AC KW ATP-binding Hydrolase; Protease; Serine protease; Mitochondrion.
Db		AC SQ SEQUENCE 950 AA; 10572 MW; D505CD851B6F07 CRC64;
Qy		AC Query Match 8.4%; Score 89; DB 11; Length 950;
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Qy		AC 104 MTHIHLDECPS -QALKVKVFAENKEIQ-O-KLAEOFVLLNLVYETTDKHLSPDGQVPRMF 161
Db		AC 262 MV--EVENTAHEDFQVTSEVKALTAEVKTIIDIANPYLERSVLMQMAGORV---- 314
Qy		AC 162 VDPSL---TVRADITGRYSNRLYAYEPADTAALLDNMKKALLKTE 205

Mon Dec 1 13:38:45 2003

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Page 7

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